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Maximum DB
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Perfect score:
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                                                       00000000
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Copyright (c) 1993 - 2000 Comp
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   AAC23183
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PT PT XX

WPI; 2000-500381/45.

Claim 1; SEQ ID 27258; 71pp + CD-ROM; English.

New nucleic acid that is a 5' expressed sequence tag (5' EST) for obtaining cDNAs and genomic DNAs that correspond to 5'ESTs and for diagnostic, forensic, gene therapy and chromosome mapping procedures

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AAC23260/c
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         identified within the present sequence. The 5' ESTs were prepared from total human RNAs or polyA+ RNAs derived from 30 different tissues. EST sequences usually correspond mainly to the 3' untranslated region (UTR) of the mRNA because they are often obtained from oligo-dT primed cDNA libraries. Such ESTs are not well suited for isolating cDNA sequences derived from the 5' ends of mRNAs and even in those cases where longer cDNA sequences have been obtained, the full 5' UTR is rarely included.
                                                                                                                 The present sequence is one of a large number of 5' ESTs derived from mRNAs encoding secreted proteins. No ORF has yet been conclusively identified within the present sequence. The 5' ESTs were prepared
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The present sequence is one of a large number of 5' ESTs derived from mRNAs encoding secreted proteins. No ORF has yet been conclusively identified within the present sequence. The 5' ESTs were prepared from total human RNAs or polyA+ RNAs derived from 30 dilferent tissues. EST sequences usually correspond mainly to the 3' untranslated region (UTR) of the mRNA because they are often obtained from oligo-dT primed cDNA libraries. Such ESTs are not well suited for isolating cDNA sequences derived from the 5' ends of mRNAs and even in those cases where longer cDNA sequences have been obtained, the full 5' UTR is rarely included. 5' ESTs are derived from mRNAs with intact 5' ends and can therefore be used to obtain full length cDNAs and genomic DNAs. 5' ESTs are also used in diagnostic, forensic, gene therapy and chromosome mapping procedures. They are used to obtain upstream regulatory sequences and to design expression and source to contain upstream regulatory sequences and to design
                                                                                                                                                                                                                                      New nucleic acid that is a 5' expressed sequence tag (5' EST) for obtaining cDNAs and genomic DNAs that correspond to 5'ESTs and fo
                                                                                                                                                                                     Claim 1; SEQ ID 27335; 71pp + CD-ROM; English
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18; Conserv
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Pred. No. 0.15;
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                                 identified within the present sequence. .... 1 different tilsues. EST total human RNAs or polyA+ RNAs derived from 30 different tilsues. EST sequences usually correspond mainly to the 3' untranslated region (UTR) of the mRNA because they are often obtained from oligo-dT primed cDNA libraries. Such ESTs are not well suited for isolating cDNA sequences derived from the 5' ends of mRNAs and even in those cases where longer CDNA sequences have been obtained, the full 5' UTR is rarely included. 5' ESTs are derived from mRNAs with intact 5' ends and can therefore be used to obtain full length cDNAs and genomic DNAs. 5' ESTs are also used in diagnostic, forensic, gene therapy and chromosome mapping procedures. They are used to obtain upstream regulatory sequences and to design
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                                                                                                                                                                                                                                                                                        New nucleic acid that is a 5' expressed sequence tag (5' EST) for obtaining cDNAs and genomic DNAs that correspond to 5'ESTs and fo
                                                                                                                                                                                                                                                  Claim 1; SEQ ID 22489;
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                                                                                                                                                                                     identified within the present sequence.
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llarity 100.0%;
Conservative (
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Pred. No. 0.15;
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Query Match
Best Local Similarity
Matches 18; Conserv

100.0%; Score 18; 100.0%; Pred. No. tive 0; Mismatch

0.15; DB 21;

Length 126;

Mismatches

0;

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Sequence 126 BP; 23 A; 49 C;

30 G;

24 T; 0 other;

and secretion

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ID AAC04894 standard; cDNA; 134
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                                                                                                                                                                                                                                           of the mRNA because they are often obtained from oligo-dy primed cDNA libraries. Such ESTs are not well suited for isolating cDNA sequences derived from the 5' ends of mRNAs and even in those cases where longer cDNA sequences have been obtained, the full 5' UTR is rarely included. 5' ESTs are derived from mRNAs with intact 5' ends and can therefore be used to obtain full length cDNAs and genomic DNAs. 5' ESTs are also used in diagnostic, forensic, gene therapy and chromosome mapping procedures. They are used to obtain upstream regulatory sequences and to design
                                                                                                                                                                                                                                                                                                                                                       The present sequence is one of a large number of 5' ESTs derived from mRNAs encoding secreted proteins. No ORF has yet been conclusively identified within the present sequence. The 5' ESTs were prepared from total human RNAs or polyA+ RNAs derived from 30 different tissues. EST sequences usually correspond mainly to the 3' untranslated region (UTR)
                                                                                                                                                                                                                                                                                                                                                                                                                                                              New nucleic acid that is a 5' expressed sequence tag (5' EST) for obtaining cDNAs and genomic DNAs that correspond to 5'ESTs and for diagnostic, forensic, gene therapy and chromosome mapping procedures
                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 1; SEQ ID 32567; 71pp + CD-ROM; English.
                                                                                                                                                                                                              Sequence 131 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Dumas Milne Edwards J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              06-SEP-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (GEST ) GENSET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          26-FEB-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  21-FEB-2000; 2000EP-0200610
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          gene therapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               06-OCT-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAC28492;
                                                                                          56
                                                                                                                                                          Local
                                                                                                              1 ggcggagcttgcagtgag 18
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                                                                                                                                              l Similarity
18; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           5' EST;
                                                                                                                                                                                                                                         and secretion
                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          chromosome mapping; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          99US-0122487
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       expressed sequence tag;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   protein 5'
                                                                                                                                                                                                           22 A; 46 C; 35 G;
                                                                                                                                                         100.0%;
                                                                                         39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Duclert A,
                                                                                                                                                                                                                                       vectors.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EST,
                                                                                                                                           0
                       ₽P.
                                                                                                                                                          Pred. No.
                                                                                                                                                                      Score 18;
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                                                                                                                                           Mismatches
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                                                                                                                                                        0.15;
                                                                                                                                                                                                             0 other
                                                                                                                                                                   DB 21;
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                                                                                                                                                                   Length 131;
                                                                                                                                           Indels
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AAC04894;

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AAC18209/c
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Best Local !
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
                                                                                      Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAC18209 standard; cDNA; 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 134 BP; 18 A; 49 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The present sequence is one of a large number of 5' ESTs derived from mRNAs encoding secreted proteins. No ORF has yet been conclusively identified within the present sequence. The 5' ESTs were prepared from total human RNAs or polyA+ RNAs derived from 30 different tissues. EST sequences usually correspond mainly to the 3' untranslated region (UTR) of the mRNA because they are often obtained from oligo-dT primed cDNA libraries. Such ESTs are not well suited for isolating cDNA sequences derived from the 5' ends of mRNAs and even in those cases where longer cDNA sequences have been obtained, the full 5' UTR is rarely included. 5' ESTs are derived from mRNAs with intact 5' ends and can therefore be used to obtain full length cDNAs and genomic DNAs. 5' ESTs are also used in diagnostic, forensic, gene therapy and chromosome mapping procedures. They are used to obtain upstream regulatory sequences and to design
                                                                                                                                                                                            gene
                                                                                                                                                                                                                                               Human;
                                                                                                                                                                                                                                                                                                                                           Human secreted
                                                                                                                                                                                                                                                                                                                                                                                                                                            06-OCT-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAC18209;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New nucleic acid that is a 5' expressed sequence tag (5' EST) for obtaining cDNAs and genomic DNAs that correspond to 5'ESTs and for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Dumas Milne Edwards J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               26-FEB-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         gene therapy;
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                                                                                                                                                                                  therapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2000-500381/45
                                                                                                                                                                   5' EST; expressed sequence tag; secreted protein; cDNA isolation; herapy; chromosome mapping; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       secreted protein 5'
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herapy; chromosome mapping; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
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                                                                                                                                                                                                                                                                                                                                 protein 5' EST,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          99US-0122487
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Duclert A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           vectors.
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Pred. No.
                                                                                                                                                                                                                                                                                                                                      SEQ ID NO: 22284
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQ ID NO:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Giordano
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AAC11987/c
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The present sequence is one of a large number of 5' ESTs derived from mRNAs encoding secreted proteins. No ORF has yet been conclusively identified within the present sequence. The 5' ESTs were prepared from total human RNAs or polyA+ RNAs derived from 30 different tissues. EST sequences usually correspond mainly to the 3' untranslated region (UTR) of the mRNA, because they are often obtained from oligo-dT primed cDNA libraries. Such ESTs are not well suited for isolating cDNA sequences derived from the 5' ends of mRNAs and even in those cases where longer CDNA sequences have been obtained, the full 5' UTR is rarely included. 5' ESTs are derived from mRNAs with intact 5' ends and can therefore be used to obtain full length cDNAs and genomic DNAs. 5' ESTs are also used in diagnostic, forensic, gene therapy and chromosome mapping procedures. They are used to obtain upstream regulatory sequences and to design expression and secretion westers.
                                                                                                                                                                                                      Human; 5' EST; expressed sequence tag;
gene therapy; chromosome mapping; ss.
          Dumas Milne Edwards J,
                                                                26-FEB-1999;
                                                                                           21-FEB-2000; 2000EP-0200610
                                                                                                                        06-SEP-2000
                                                                                                                                                    EP1033401-A2
                                                                                                                                                                               Homo sapiens
                                                                                                                                                                                                                                                 Human secreted protein 5' EST, SEQ ID NO: 16062
                                                                                                                                                                                                                                                                                06-OCT-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 135 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 1; SEQ ID 22284; 71pp + CD-ROM; English.
                                       (GEST ) GENSET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 expression and secretion
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                                                                                                                                                                                                                                                                                                                                                                                                             107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity hes 18; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                       1 ggcggagcttgcagtgag 18
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                                                                                                                                                                                                                                                                           (first entry)
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                                                                                                                                                                                                                                                                                                                                      CDNA; 138
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   35 C;
          Duclert A,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                0;
                                                                                                                                                                                                                                                                                                                                      ВP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 18;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    <u>ن</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    44 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Giordano
       Giordano J;
                                                                                                                                                                                                                  secreted protein; cDNA isolation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0.15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        21; Length 135;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               0,
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                                                                                                                                                                         Matches
                                                                                                                                                                                                                       total human RNAs or polyA+ RNAs derived from 30 different tissues. EST sequences usually correspond mainly to the 3' untranslated region (UTR) of the mRNA because they are often obtained from oligo-dT primed cDNA libraries. Such ESTs are not well suited for isolating cDNA sequences derived from the 5' ends of mRNAs and even in those cases where longer cDNA sequences have been obtained, the full 5' UTR is rarely included. 5' ESTs are derived from mRNAs with intact 5' ends and can therefore be used to obtain full length cDNAs and genomic DNAs. 5' ESTs are also used in diagnostic, forensic, gene therapy and chromosome mapping procedures. They are used to obtain upstream regulatory sequences and to design expression and correction workers.
                                                                                                                                                                         Sequence 138
                                                                                                                                                                                                                                                                                                                                                                                                                         The present sequence is one of a large number of 5' E: mRNAs encoding secreted proteins. No ORF has yet been identified within the present sequence. The 5' ESTs we
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 1; SEQ ID 16062; 71pp + CD-ROM; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       diagnostic, forensic, gene therapy and chromosome mapping procedures
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New nucleic acid that is a 5' expressed sequence tag (5' EST) obtaining cDNAs and genomic DNAs that correspond to 5'ESTs and
                                                                                                                                                                                                               expression and secretion vectors.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2000-500381/45
75 GGCGGAGCTTGCAGTGAG 58
                                                                                             Local
                   1 ggcggagcttgcagtgag
                                                                             18;
                                                                                             Similarity
                                                                           Conservative
                                                                                                                                                                         BP;
                                                                                                                                                                         21
                                                                                                                                                                     A; 47 C; 34 G;
                                                                                           100.0%;
                                   18
                                                                           0
                                                                                           Score 18; DB 2
Pred. No. 0.15;
                                                                         Mismatches
                                                                                                                                                                     35 T; 1 other;
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                                                                                                                                                                                                                                                                                                                                                                                                                       ESTs were prepared from
                                                                                                         Length 138;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             ESTs derived
                                                                                                                                                                                                                                                                                                                                                                                                                                             conclusively
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                                                                       Gaps
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RESULT 8
AAC15609/c
                                                                                                                                             06-SEP-2000.
WPI; 2000-500381/45.
                         Dumas Milne Edwards J,
                                                         (GEST ) GENSET
                                                                                     26-FEB-1999;
                                                                                                                21-FEB-2000; 2000EP-0200610
                                                                                                                                                                          EP1033401-A2
                                                                                                                                                                                                      Homo sapiens
                                                                                                                                                                                                                                 gene therapy;
                                                                                                                                                                                                                                                    Human; 5' EST;
                                                                                                                                                                                                                                                                                                          06-OCT-2000
                                                                                                                                                                                                                                                                                                                                                                 AAC15609 standard; cDNA; 138
                                                                                                                                                                                                                                                                             Human secreted
                                                                                                                                                                                                                                                                                                                                       AAC15609
                                                                                                                                                                                                                                                                                                         (first entry)
                                                                                                                                                                                                                                ; expressed sequence tag;
chromosome mapping; ss.
                                                                                     99US-0122487
                                                                                                                                                                                                                                                                             protein 5'
                         Duclert A,
                                                                                                                                                                                                                                                                             EST,
                                                                                                                                                                                                                                                                                                                                                                   ВP
                                                                                                                                                                                                                                                                             SEQ ID
                         Giordano J;
                                                                                                                                                                                                                                                                             NO: 19684.
                                                                                                                                                                                                                                            secreted protein; cDNA isolation;
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CCCCXXX

The present sequence is one of a large number of 5' ESTs derived from mRNAs encoding secreted proteins. No ORF has yet been conclusively identified within the present sequence. The 5' ESTs were prepared from

ESTs were prepared from

New nucleic acid that is a 5' expressed sequence tag (5' EST) for obtaining cDNAs and genomic DNAs that correspond to 5'ESTs and for diagnostic, forensic, gene therapy and chromosome mapping procedures

Claim

1; SEQ

ID 19684; 71pp + CD-ROM; English.

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Query Match
Best Local S
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mRNAS encoding secreted proteins. No ORF has yet been conclusively identified within the present sequence. The 5' ESTs were prepared from total human RNAs or polyA+ RNAs derived from 30 different tissues. EST sequences usually correspond mainly to the 3' untranslated region (UTR) of the mRNA because they are often obtained from oligo-dT primed cDNA libraries. Such ESTs are not well suited for isolating cDNA sequences derived from the 5' ends of mRNAs and even in those cases where longer CDNA sequences have been obtained, the full 5' UTR is rarely included. 5' ESTs are derived from mRNAs with intact 5' ends and can therefore be used to obtain full length cDNAs and genomic DNAs. 5' ESTs are also used in diagnostic, forensic, gene therapy and chromosome mapping procedures. They are used to obtain upstream regulatory sequences and to design
                                                                                                                                                                                                                                                                                                                                                                         New nucleic acid that is a 5' expressed sequence obtaining cDNAs and genomic DNAs that correspond diagnostic, forensic, gene therapy and chromosome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            total human RNAs or polyA+ RNAs derived from 30 different tissues. EST sequences usually correspond mainly to the 3' untranslated region (UTR) of the mRNA because they are often obtained from oligo-dT primed cDNA libraries. Such ESTs are not well suited for isolating cDNA sequences derived from the 5' ends of mRNAs and even in those cases where longer cDNA sequences have been obtained, the full 5' UTR is rarely included. 5' ESTs are derived from mRNAs with intact 5' ends and can therefore be used to obtain full length cDNAs and genomic DNAs. 5' ESTs are also used in diagnostic, forensic, gene therapy and chromosome mapping procedures. They are used to obtain upstream regulatory sequences and to design
                                                                                                                                                                                                                                                                                   The present sequence is one of a large number of 5' ESTs derived
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2000-500381/45
                                                                                                                                                                                                                                                                                                                                            Claim
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      26-FEB-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 138 BP; 36 A; 36 C; 36 G;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     therapy;
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                                                                                                                                                                                                                                                                                                                                            SEQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          protein 5'
                                                                                                                                                                                                                                                                                                                                       19765;
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                                                                                                                                                                                                                                                                                                                                   71pp + CD-ROM; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Duclert A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  mapping;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     vectors.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EST,
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Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQ ID NO: 19765
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Giordano
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                                                                                                                                                                                                                                                                                                                                                                                   chromosome
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           21;
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                                                                                                                                                                                                                                                                                                                                                                           mapping
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                                                                                                                                                                                                                                                                                                                                                                              procedures
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В Ş

99 -

ggcggagcttgcagtgag

82

Query Match Best Local S Matches 18

l Similarity 18; Conserv

Conservative

0;

Mismatches

0;

Indels

0;

Gaps

0

100.0%;

Score 18; DB 2 Pred. No. 0.14;

21;

Length 167;

Sequence 167

BP;

21 A; 58 C;

35 G;

48

T; 5 other

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RESULT 10
AAC05392/c
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Matches 18; Conserv
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                     The present sequence is one of a large number of 5' ESTs derived from mRNAs encoding secreted proteins. No ORF has yet been conclusively identified within the present sequence. The 5' ESTs were prepared from total human RNAs or polyA+ RNAs derived from 30 different tissues. EST sequences usually correspond mainly to the 3' untranslated region (UTR) of the mRNA because they are often obtained from oligo-dT primed cDNA libraries. Such ESTs are not well suited for isolating cDNA sequences derived from the 5' ends of mRNAs and even in those cases where longer cDNA sequences have been obtained, the full 5' UTR is rarely included. 5' ESTs are derived from mRNAs with intact 5' ends and can therefore be used to obtain full length cDNAs and genomic DNAs. 5' ESTs are also used in diagnostic, forensic, gene therapy and chromosome mapping procedures. They are used to obtain upstream regulatory sequences and to design expression and secretion vectors.
                                                                                                                                                                                                                     Claim 1;
                                                                                                                                                                                                                                                      New nucleic acid that is a 5' expressed sequence obtaining cDNAs and genomic DNAs that correspond
                                                                                                                                                                                                                                                                                                                         Dumas Milne Edwards
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                                                                                                                                                                                                                                                                                                                                                    (GEST ) GENSET
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                                                                                                                                                                                                                   SEQ ID 9467;
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                                                                                                                                                                                                                                             forensic,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       chromosome mapping;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  expressed sequence tag;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             protein 5' EST,
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                                                                                                                                                                                                                                             gene
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Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQ ID NO: 9467.
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                                                                                                                                                                                                                                                                                                                      Giordano
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                                                                                                                                                                                                                                       chromosome mapping procedures
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  protein; cDNA isolation
                                                                                                                                                                                                                                                      tag (5' EST) for to 5'ESTs and fo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 151;
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                                                                                                     RESULT 12
AAC04655/c
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                                                                                                                                                                                                                                                                                               RESULT
AAC11951
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Best Local 9
                                                                                                                                                                                                                         Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New nucleic acid that is a 5' expressed sequence tag (5' I obtaining cDNAs and genomic DNAs that correspond to 5'ESTs diagnostic, forensic, gene therapy and chromosome mapping
 Human secreted protein 5'
                                                                                                                                                                                                                                                                                            Sequence 172 BP; 51 A; 45 C; 53 G;
                                                                                                                                                                                                                                                                                                                                    used to obtain full length cDNAs and genomic DNAs. 5' ESTs are also used in diagnostic, forensic, gene therapy and chromosome mapping procedures. They are used to obtain upstream regulatory sequences and to design
                              06-OCT-2000
                                                          AAC04655;
                                                                                    AAC04655 standard; cDNA; 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 1; SEQ ID 16026; 71pp + CD-ROM; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2000-500381/45.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (GEST ) GENSET
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human; '5' EST; expressed sequence tag;
gene therapy; chromosome mapping; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human secreted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          06-OCT-2000
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                                                                                                                                                                87
                                                                                                                                                                                                                       Local Similarity hes 18; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  11
                                                                                                                                                                          1 ggcggagcttgcagtgag 18
                                                                                                                                                           ggcggagcttgcagtgag 104
                                                                                                                                                                                                                                                                                                                           and secretion vectors.
                                                                                                                                                                                                                    100.0%; ilarity 100.0%; Conservative (
                           (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               9905-0122487
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   J,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    172
 EST,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EST,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BP
                                                                                                                                                                                                                                Score 18; DB 2:
Pred. No. 0.14;
SEQ ID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQ ID NO: 16026
                                                                                                                                                                                                                       Mismatches
                                                                                                                                                                                                                                                                                            23 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Giordano J;
ŏ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            secreted protein; cDNA isolation;
                                                                                                                                                                                                                                                DB 21;
                                                                                                                                                                                                                    0;
                                                                                                                                                                                                                                              Length 172;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        tag (5' EST) for to 5'ESTs and for
                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           procedures
                                                                                                                                                                                                                    0;
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Query Match
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Matches 18
                                                                                                                                                                                                                                libraries. Such ESTs are not well suited for isolating cDNA sequences derived from the 5' ends of mRNAs and even in those cases where longer cDNA sequences have been obtained, the full 5' UTR is rarely included. 5' ESTs are derived from mRNAs with intact 5' ends and can therefore be used to obtain full length cDNAs and genomic DNAs. 5' ESTs are also used in diagnostic, forensic, gene therapy and chromosome mapping procedures. They are used to obtain upstream regulatory sequences and to design
                                                                                                                                                                                                                                                                                                                                                                                                                                     The present sequence is one of a large number of 5' ESTs derived from mRNAs encoding secreted proteins. No ORF has yet been conclusively identified within the present sequence. The 5' ESTs were prepared from total human RNAs or polya+ RNAs derived from 30 different tissues. EST sequences usually correspond mainly to the 3' untranslated region (UTR) of the mRNA because they are often obtained from oligo-dT primed cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI;
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                                                                                                                                                 Sequence 182 BP; 22 A; 46 C; 35 G; 78 T; 1 other;
                                                                                                                                                                                                           expression and secretion vectors.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 1; SEQ ID 8730; 71pp + CD-ROM; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New nucleic acid that is a 5' expressed sequence tag (5' EST) for obtaining cDNAs and genomic DNAs that correspond to 5'ESTs and for diagnostic, forensic, gene therapy and chromosome mapping procedu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Dumas Milne Edwards J,
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         Local Similarity
nes 18; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      5' EST; expressed sequence tag;
   100.0%;
ilarity 100.0%;
Conservative (
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         0
                                 Score 18;
Pred. No.
      Mismatches
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                                 0.14;
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                                                         Length 182;
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Gaps
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18
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AAC16191 standard; cDNA; 185 BP
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RESULT
                                                                                   AAC16191
 Human secreted protein 5' EST,
                         06-OCT-2000
                                                AAC16191;
                       (first entry)
SEQ ID
 NO: 20266
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X P X A

Homo sapiens

Human; 5' EST;
gene therapy; (

chromosome

expressed

sequence tag; secreted protein; cDNA isolation; mapping; ss.

21-FEB-2000; 2000EP-0200610.

06-SEP-2000 EP1033401-A2

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Matches 18
                                WPI; 2000-500381/45
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                                                                                                                                                                                                                                                                                                                                        AAC22610 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                of the mRNA because they are often obtained from oligo-dT prined cDNA libraries. Such ESTs are not well suited for isolating cDNA sequences derived from the 5' ends of mRNAs and even in those cases where longer cDNA sequences have been obtained, the full 5' UTR is rarely included. 5' ESTs are derived from mRNAs with intact 5' ends and can therefore be in diagnostic, forensic, gene therapy and chromosome mapping procedures. They are used to obtain upstream regulatory sequences and to design expression and secretion vectors.
                                                         Dumas Milne Edwards
                                                                                 (GEST ) GENSET
                                                                                                         26-FEB-1999;
                                                                                                                                21-FEB-2000;
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                                                                                                                                                                                                       Homo sapiens
                                                                                                                                                                                                                                gene
                                                                                                                                                                                                                                                                Human secreted protein 5'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 185 BP; 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Identified within the present sequence. The 5' ESTs were prepared total human RNAs or polyA+ RNAs derived from 30 different tissues sequences usually correspond mainly to the 3' untranslated region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The present sequence is one of a large number of 5' ESTs derived mRNAs encoding secreted proteins. No ORF has yet been conclusivel identified within the present sequence. The 5' ESTs were prepared total human RNAs or polyA+ RNAs derived from 30 different tissues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New nucleic acid that is a 5' expressed sequence obtaining cDNAs and genomic DNAs that correspond
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                                                                                                                                                                                                                             therapy;
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                                                                                                                                                                                                                                          5' EST;
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                                                                                                                               2000EP-0200610
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                                                                                                                                                                                                                           chromosome mapping;
                                                                                                        99US-0122487
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                                                                                                                                                                                                                                                                                                                                        cDNA; 186
                                                        'n
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                                                                                                                                                                                                                                                               SEQ ID NO: 26685
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                                                                                                                                                                                                                             SS.
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                                                      Giordano
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                                                                                                                                                                                                                                      protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 185;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           mapping procedures
                                                                                                                                                                                                                                      cDNA isolation;
                                                                                                                                                                                                                                                                                                                                                                                                                                              0;
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New nucleic acid that obtaining cDNAs and

acid that is a 5' expressed sequence tag (5' EST) for DNAs and genomic DNAs that correspond to 5'ESTs and for

The present sequence is one of a large number of 5' ESTs derived from mRNAs encoding secreted proteins. No ORF has yet been conclusively identified within the present sequence. The 5' ESTs were prepared from total human RNAs or polyA+ RNAs derived from 30 different tissues. EST sequences usually correspond mainly to the 3' untranslated region (UTI

ESTs were prepared from

(UTR)

are often obtained from oligo-dT not well suited for isolating cD

New nucleic acid that is a 5' expressed sequence tag (5' EST) for obtaining cDNAs and genomic DNAs that correspond to 5'ESTs and for diagnostic, forensic, gene therapy and chromosome mapping procedure

procedures

Claim 1; SEQ

ID 26546;

71pp + CD-ROM; English.

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RESULT 15
AAC22471/c
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The present sequence is one of a large number of 5' ESTs derived mRNAs encoding secreted proteins. No ORF has yet been conclusive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   118
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        diagnostic,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 ggcggagcttgcagtgag
                                                                                                                                                                                                                                                                                                                                                                                                  sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                             therapy;
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Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
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                                                                                                                                                                                                                           Giordano
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                                                                                                                                                                                                                                                                                                                                                                                                                                          protein;
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                                                                                                                                                                                                                                                                                                                                                                                                                                         cDNA isolation;
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to design
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Result
No.
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Maximum DB seq length: 2000000000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Perfect score:
Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Post-processing: Listing first 45 summaries
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                                                                                                                                                                                                                                                                                                                                             score greater than and is derived by a
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B. burgdorferi ant
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Arabidopsis thalia
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dopsis t	olon cancer asso	C. elegans SPE-4 D	0	Human PPAR-gamma-2	Human secreted pro	Riboflavin 1 gene	N. tabacum CYCD3;1	breast c	PRO1864	PDGF receptor beta	PRLTS coding seque	3	secreted p	PPARqamm.	secreted pr	breast	Human breast cance	Extended human sec	ĊŤ.		gene ex	-	Arabidopsis thalia	α.	secret	prostate	secreted p	TANGO 187-	TANGO 187	TANGO 187-	TANGO 187-	TANGO 187	Human TANGO 187-2	

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03-SEP-1997;
20-JUN-1997;
22-JUL-1997;
22-JUL-1997;
             WPI; 1999-189980/16.
P-PSDB; AAY19875.
                                    Choi GH,
                                                                                                                                                                          Antigenic protein; vaccine; Lyme disease; infection; detection; ss
                                                                                                                                                                                         B. burgdorferi antigenic protein coding sequence, t617.nt
                                                                                                                                30-DEC-1998
                                                                                                                                              WO9859071-A1.
                                                                                                                                                                                                         19-JUL-1999 (first entry)
                                                   (HUMA-) HUMAN GENOME SCI INC (MEDI-) MEDIMMUNE INC.
                                                                                                                                                            Borrelia burgdorferi.
                                                                                                                                                                                                                            AAX61572;
                                                                                                                18-JUN-1998;
                                  Erwin AL,
                                                                         97US-0057483.
97US-0050359.
97US-0053344.
97US-0053377.
                                                                                                                98WO-US12718
                                   Hanson MS,
                                  Lathigra
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New isolated Borrelia burgdorferi nucleic acids

used to develop

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20-JUN-1997;
22-JUL-1997;
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                                                                                 This sequence encodes a Borrelia burgdorferi (Bb) protein invention, which is suitable for use in a vaccine. The Bb
                                                                                                                                                                                                                                  Choi GH,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              B. burgdorfer1 antigenic protein coding sequence, f617.nt
 Sequence
                                                                                                                         Claim 1;
                                                                                                                                            New isolated Borrelia burgdorferi nucleic acids - us products for the diagnosis, prevention and treatment caused by Borrelia, particularly Lyme disease
                                                                                                                                                                                                                                                                                                                                                          18-JUN-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   can be used in vaccines for eliciting protective antibodies to members of the Borrelia genus, particularly for the use against Lyme disease in humans and animals. They can be used for preventing or attenuating an infection caused by a member of the Borrelia genus. The products can also be used for detection of members of the Borrelia genus.
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                                     infection
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                       ention, which is suitable for use in a vaccine. The Bb polypeptides be used in vaccines for eliciting protective antibodies to members Borrelia genus, particularly for the use against Lyme disease in ans and animals. They can be used for preventing or attenuating an ection caused by a member of the Borrelia genus. The products can alused for detection of members of the Borrelia genus.
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y Borrelia, particu
                                                                                                                        Page
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                                                                                                                                                                                                                                  Erwin AL,
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A; 90 C;
                                                                                                                                                                                                                                   Hanson
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                                                                                                                       English.
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0 other;
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                                                                                                                                                                                                                                                         production of biosynthetic products, e.g. enzymes. Borrelia belongs
to a family of motile, spiral-shaped bacteria called Spirochetes.
Spirochetes are pathogenic in humans and Borrelia causes epidemic and
endemic relapsing fever, and Lyme borreliosis, more commonly known as
                                                                                                                                                                                               Sequence
                                                                                                                                                                                                                                       Lуme
                                                                                                                                                                                                                                                                                                                                          Borrelia burgdorferi (Bb). Products derived from Bb can be used for
the detection, diagnosis, characterisation, prevention and therapy of
Bb infections, e.g. Lyme disease. They can also be used for the
                                                                                                                                                                                                                                                                                                                                                                                                             AAX20248
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              and therapy of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New isolated Borrella burgdorferi nucleic acids - used to products for the detection, diagnosis, characterisation,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 1999-081217/07.
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20-JUN-1997;
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22-JUL-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      Page 157-671; 1128pp; English.
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llarity 100.0%;
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ever; Lyme borreliosis;
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RESULT
AAC50076
                                                                                        Query Match
Best Local Similarity 100...
"atches 15; Conservative
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                                                                                                                                                                                 stromal lymphopoietin (TSLP). It was isolated by searching an EST library for sequences similar to the murine TSLP sequence. The protein is involved in the growth and differentiation of B and T cells. It can be used to study processes such as immune regulation, cell interaction and inflammatory responses. The nucleic acid can be used to identify human chromosome b, to map genes along this chromosome, to identify genes on this chromosome which are associated with diseases, including Gardner syndrome and colorectal cancer, and to inhibit or induce B and T cell
                  AAC50076 standard; DNA; 1310
                                                                                                                                                                                                                                                                                    The present sequence is the coding sequence for human
                                                                                                                                                                                                                                                                                                                         New human thymic stromal lymphopoietin (TSLP) polypeptide useful for stimulating lymphocyte development and proliferation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human; thymic stromal lymphopoletin; TSLP; B cell maturation; immune regulation; cell proliferation; cell differentiation; cell decell migration; cell-to-cell interaction; inflammatory response; chromosome 5q21-22; Gardner syndrome; adenomatous polyposis coll; hereditary desmoid disease; Turcot syndrome; colorectal cancer; ss.
                                                                  4 gatttattttgggct 18
|||||||||||||||
721 GATTTATTTTGGGCT 707
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Pred. No
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14-MAY-1999;
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24 - JUN - 1999; 28 - JUN - 1999; 23-JUN-1999; 23-JUN-1999; 21-JUN-1999; 22-JUN-1999;

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29-SEP-1999
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08-OCT-1999
Hybridisation assay; genetic mapping; gene expression control;
                   Arabidopsis thaliana DNA fragment SEQ ID NO: 18660
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10-SEP-1999;
13-SEP-1999;
               W09929870-A1
                             Porphorymonas gingivalis.
                                                                  Porphorymonas gingivalis protein PG7 ORF encoding DNA.
                                                                                                                   AAX91624 standard; DNA; 1392 BP
17-JUN-1999
                                             Porphorymonas gingivalis; PG; periodontal disease; gingivitis; vaccine; antigenic; ds.
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0; Mismatches
                                                                                                                                                                                                         21; Length 1313;
                                                                                                                                                                                          0;
                                                                                                                                                                                          Indels
                                                                                                                                                                                         0;
                                                                                                                                                                                          Gaps
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                                                                                                                                                                                                                                                                         RESULT
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                        Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    04 - AUG-1998
10 - DEC-1997
31 - DEC-1997;
31 - JAN-1998
10 - AUR-1998
10 - AUR-1998
09 - AUR-1998
23 - AUR-1998
22 - AUX-1998
29 - JUL-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                  AAX91536 to AAX91801 encode two hundred and sixty six antigenic Porphorymonas gingivalis (PG) polypeptide sequences given in AAX34318 to AAX914583. AAX91802 to AAX91989 represent PCR primers used in the isolation of the PG polypeptides. The PG polypeptides have antibacterial activity with a vaccine mechanism of action. The PG polypeptides can be used as vaccines especially against Porphorymonas gingivalis. Probes can be used to detect Porphorymonas gingivalis in standard hybridisation assays. Porphorymonas gingivalis is involved in periodontal disease especially gingivitis.
                               sig_peptide
                                                                   CDS
                                                                                                    Homo sapiens.
                                                                                                                                        Human T1-receptor ligand III; T1-R ligand III; atherosclerosis; autoimmune disease; inflammation; metabolic dysfunction;
                                                                                                                                                                      Human T1-receptor ligand III splice variant 1 encoding cDNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Agius CT,
Ross BC,
                                                                                                                                                                                                  10-DEC-1998
                                                                                                                                                                                                                         AAV33461;
                                                                                                                                                                                                                                                AAV33461 standard; cDNA; 1836 BP
                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 1392 BP; 361 A; 311 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 12; Page 156; 588pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Antigenic Porphorymonas gingivalis peptides for preventing gingivitis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 1999-385613/32.
P-PSDB; AAY34406.
                                                                                                                            immune-regulated disorder; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      10-DEC-1998;
                                                                                                                                                                                                                                                                                                        1 tcagatttattttgg 15
||||||||||||||
56 tcagatttattttgg 70
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Rothel LJ,
                                                                                                                                                                                                                                                                                                                                             ularity 100.0%; Score 15;
Conservative 0; Mix.
                                                                                                                                                                                               (first entry)
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97AU-0001823
97AU-0001182
98AU-0001546
98AU-0002564
98AU-0002911
98AU-0003128
98AU-0003538
98AU-0003534
98AU-0004917.
                  /product=
31..102
/*tag= b
       /*tag- k
103..519
                                                                 Location/Qualifiers 31..522
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      98WO-AU01023
                                                        /*tag=
                                                                                                                                      inflammation; metabolic dysfunction;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hocking DM,
Webb EA;
                                                      a
                                          "T1-R ligand III splice variant 1"
                                                                                                                                                                                                                                                                                                                                                       Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                328 G;
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                                                                                                                                                                                                                                                                                                                                                                                                                392 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                               DB
                                                                                                                                                                                                                                                                                                                                                                             20; Length 1392;
                                                                                                                                                                                                                                                                                                                                                       0;
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mat_peptide

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RESULT
AAF93852
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                       Matches
                                                           08-JUL-1999;
11-JAN-2000;
02-MAY-2000;
                                                                                                                                                                                 Human; secretory protein; membrane protein; rheumatoid arthritis; diabetes; ss.
                    Ota T,
                                                                                                07-JUL-2000; 2000EP-0114090
                                                                                                                      10-JAN-2001
                                                                                                                                                                                                                                                                           AAF93852 standard; cDNA; 2083 BP
WPI; 2001-093989/11
                                                                                                                                           EP1067182-A2
                                                                                                                                                              Homo sapiens
                                                                                                                                                                                                                 Human cDNA
                                                                                                                                                                                                                                     23-MAY-2001
                                                                                                                                                                                                                                                         AAF93852;
                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 1836 BP; 637 A; 306 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 2; Fig 1; 115pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New human T1-receptor ligand III splice variant(s) e.g. detecting and treating immune system related cancer and inflammation
                                       (HELI-) HELIX RES INST.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              proteins.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (HUMA-) HUMAN GENOME SCI INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           26-FEB-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    variant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       28-FEB-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               03-SEP-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   W09838311-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                          immune-regulated disorders.
                                                                                                                                                                                                                                                                                                                               981
                                                                                                                                                                                                                                                                                                                                                                                                                                                    utoimmune disease, inflammation,
                                                                                                                                                                                                                                                                                                                                                                                                                                                  seful for screening agonists and antagonists. They are also laimed useful for treating disorders such as atherosclerosis, utoimmune disease, inflammation, metabolic dysfunction and
                                                                                                                                                                                                                                                                                                                                        1 tcagatttattttgg
                                                                                                                                                                                                                                                                                                9
                                                                                                                                                                                                                                                                                                                             tcagatttattttgg 995
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DB; AAW70458.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       III)
                   Isogai T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             tion provides novel human T1-receptor ligand III (T1-R) splice variants and antibodies raised against these The present cDNA encodes the T1-R ligand III splice protein. The T1-R ligand III splice variants are claimed
                                                                                                                                                                                                            encoding a membrane or secretory protein clone PSEC0198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ni J,
                                                          99JP-0194179.
2000JP-0118775.
2000JP-0183766.
                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                   (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      97US-0039483
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           98WO-US03483
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ruben SM;
                   Nishikawa
                                                                                                                                                                                                                                                                                                                                                 15
                                                                                                                                                                                                                                                                                                                                                                                100.0%;
                                                                                                                                                                                                                                                                                                                                                                                         62.5%;
                                                                                                                                                                                                                                                                                                                                                                     0;
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Pred. No.
                   'n
                                                                                                                                                                                                                                                                                                                                                                    Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                      353 G;
                  Kawai Y,
                                                                                                                                                                                                                                                                                                                                                                                                                      540 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                             15;
                Sugiyama
                                                                                                                                                                                                                                                                                                                                                                                       19;
                                                                                                                                                                                        vaccine; gene therapy
                                                                                                                                                                                                                                                                                                                                                                   0;
                                                                                                                                                                                                                                                                                                                                                                                       Length 1836;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                disorders
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                Ŧ,
               Hayashi
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                                                                                                                                                                                                                                                                                                                                                                   0;
                <u>~</u>
                                                                                                                                                                                                                                                                                                                                                                   Gaps
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CDS

Location/Qualifiers 386..1135 /*tag= a /product= "TANGO 187

/*tag=

Homo sapiens.

WO200018904-A2

30-SEP-1998; 30-SEP-1999; 06-APR-2000

98US-0164220 99WO-US22817

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local :
                                                                                                                                                                                                                                             TANGO 180; TANGO 181; TANGO 182; TANGO 183; TANGO 184; TANGO 186; TANGO 188; TANGO 189; TANGO 215; TANGO 187; secreted protein; transmembrane protein; gene therapy; diagnosis; treatment; detection; ss.
                                                                                                                                                                                                                                                                                                                                     Human TANGO 187 cDNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1309
                                                                                                                                                                                                                                                                                                                                                                                                          AAA39981;
                                                                                                                                                                                                                                                                                                                                                                                                                                        AAA39981 standard; cDNA; 2385
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (e.g. polymerase chain reactions (PCR)) to detect and quantitate the presence of similar nucleic acid sequences in samples. They may also be used to study the expression and function of secretory proteins/membrane polypeptides and their role in metabolism. The polypeptides may be used as antigens in the production of antibodies against them and in assays to identify modulators (agonists and antagonists) of expression and
                                                                                                                                                                                                                                                                                                                                                                       16-OCT-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       cDNA sequences of the invention. The invention also includes methods for the production of antibodies directed against the proteins, and cDNA sequences, which can be used in vaccines. The polynucleotide sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 2083 BP; 544 A; 467 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    arthritis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              be used as diagnostic agents for detecting the presence of the polypeptides in samples (e.g. by enzyme linked immunosorbant assay (ELISA). Examples of diseases which may be treated include rheumat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            activity. The antibodies and antagonists may also be used as therapeutic agents to down regulate expression and activity. The antibodies may also
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  protein/membrane protein expression. The nucleic acids and complementary sequences may also be used as DNA probes in diagnostic assays
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   can be used in gene therapy. The polynucleotide sequences and the proteins they encode may be used in the prevention, treatment and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This invention relates to nucleic acid sequences AAF93744 - AAF93916 which encode human secretory or membrane proteins represented by AAB88317 - AAB88419. Included in the invention are primers AAF939917 - AAF94295 and AAF62232 - AAF62235 which are used to isolate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Nucleic acids encoding secretory proteins/membrane proteins, useful in gene therapy or as candidate target molecules in drug development - \,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       diagnosis of diseases associated with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 1; SEQ ID 217; 609pp + CD ROM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     P-PSDB; AAB88425
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 tcagatttattttgg 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           tcagatttattttgg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            l Similarity 100
15; Conservative
                                                                                                                                                                                                                                                                                                                                                                     (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1323
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               62.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              .0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 15;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               491 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     inappropriate secretory
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               581 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB
15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              be treated include rheumatoid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 2083;
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                                                                                                                                                                                                                                                                 TANGO 185;
human; murine;
vaccine;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          for
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02-OCT-1998;

98US-0164169

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CC This invention describes novel human and murine nucleic acids encoding CC TANGO polypeptides (which are either wholly secreted or transmembrane proteins) which can be used for gene therapy and/or vaccination. The CC peptides are designated TANGO 180 to TANGO 189 and TANGO 215. The nucleic acids may be used to produce TANGO 180 to TANGO 189 and TANGO 215. The nucleic comparation of the produce TANGO 180 to TANGO 189 and TANGO 215. The nucleic comparation of the produce TANGO 180 to TANGO 189 and TANGO 215. The nucleic comparation of the produce TANGO 180 to TANGO 189 and TANGO 180 nucleic comparation are used to detect and quantify the presence of TANGO nucleic comparation are presented to over or comparation of the polypeptides or the expression of inactive polypeptides). The nucleic acids and the polypeptides they encode may be used according to standard gene therapy protocols, to treat diseases associated with inappropriate TANGO expression by supplementing a comparation of the polypeptide of to rectify mutations that the polypeptide of to rectify mutations that comparation of the polypeptide of to rectify mutations that compared the polypeptide of 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           may result in expression of an abnormally active polypeptide. The polypeptides may also be used to identify and produce agonists and antagonists of TANGO expression and activity which may be used to modulate TANGO related processes and diseases. The polypeptides are particularly useful for use as antigens for producing antibodies to TANGO proteins which may be used for inhibiting the activity of TANGO proteins. They may also be used to detect and quantify the presence of TANGO proteins in samples and therefore identify patients in whom the protein is over- or under-expressed. This sequence encodes the human TANGO 187 protein described in the method of the invention.
                                                                                                                                                                                                                                    TANGO 180; TANGO 181; TANGO 182; TANGO 183; TANGO 184; TANGO 185; TANGO 186; TANGO 188; TANGO 189; TANGO 215; TANGO 187; human; muj
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1279 tcagatttattttgg 1293
                                                                                                                                                                                             diagnosis; treatment;
                                                                                                                                                                                                                   secreted protein; transmembrane protein;
                                                                                                                                                                                                                                                                                                                              Human TANGO 187-1/3 cDNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAA39953 standard; cDNA; 2403 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 2385 BP; 623 A; 519 C;
                                                                                                                                          Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                       16-OCT-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                               AAA39953;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Disclosure; Fig 52; 249pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Isolated nucleic acids encoding TANGO polypeptides useful for preventing, diagnosing and treating diseases associated with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           inappropriate protein expression
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 tcagatttattttgg 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
                         /*tag=
                                                     Location/Qualifiers
     /product=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      62.5%; Score 15; 100.0%; Pred. No.
                                                                                                                                                                                       detection; ss.
"TANGO 187-1/3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           588 G; 653 T; 2 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB
                                                                                                                                                                                                                gene therapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            21; Length 2385;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                           numan; murine;
vaccine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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CC may also be used to detect and quantify the presence of TANGO nucleic CC acids in a sample and therefore identify or diagnose diseases associated CC with inappropriate TANGO expression (e.g. diseases related to over or CC under expression of the polypeptides or the expression of inactive CC polypeptides). The nucleic acids and the polypeptides they encode may be CC used according to standard gene therapy protocols, to treat diseases CC associated with inappropriate TANGO expression by supplementing a CC may result in expression of an abnormally active polypeptide. The CC may result in expression of an abnormally active polypeptide. The CC polypeptides may also be used to identify and produce agonists and CC antagonists of TANGO expression and activity which may be used to compare toward to the compare of the polypeptide of the polypeptide of the polypeptide of the polypeptide of the compared to the compared to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This invention describes novel human and murine nucleic acids encoding TANGO polypeptides (which are either wholly secreted or transmembrane proteins) which can be used for gene therapy and/or vaccination. The peptides are designated TANGO 180 to TANGO 189 and TANGO 215. The nucle acids may be used to produce TANGO 180 to TANGO 189 and TANGO 215 polypeptides according to standard recombinant DNA methodologies. They
Sequence 2403 BP; 660 A; 504 C; 566 G; 673 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 1c; Fig 20; 249pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Isolated nucleic acids encoding TANGO polypeptides useful for preventing, diagnosing and treating diseases associated with inappropriate protein expression -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WO200018904-A2
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02-OCT-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (MILL-) MILLENNIUM BIOTHERAPEUTICS INC
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98US-0164169
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Best Local Similarity
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TANGO 180; TANGO 181; TANGO 182; TANGO 183; TANGO 184; TANGO 186; TANGO 188; TANGO 189; TANGO 215; TANGO 187; secreted protein; transmembrane protein; gene therapy;
                                                                                                                                                          1285 tcagatttattttgg 1299
                                             Human TANGO 187-2 cDNA
                                                                 16-OCT-2000
                                                                                       AAA39979;
                                                                                                         AAA39979 standard; cDNA; 2418
                                                                                                                                                                                1 tcagatttattttgg 15
                                                                                                                                                                                                      Conservative
                                                               (first entry)
                                                                                                                                                                                                                62.5%;
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                                                                                                                                                                                                                 Score 15;
Pred. No.
                                                                                                                                                                                                     Mismatches
                                                                                                                                                                                                               15;
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                                                                                                                                                                                                                         Length 2403;
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                     TANGO 185;
          human; murine;
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vaccine;

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                                                                                                                                                                                                                                                  CC polypeptides according to standard recombinant DNA methodologies. They C acids in a sample and therefore identify the presence of TANGO nucleic CC acids in a sample and therefore identify or diagnose diseases associated CC with inappropriate TANGO expression (e.g. diseases related to over or CC under expression of the polypeptides or the expression of inactive polypeptides). The nucleic acids and the polypeptides they encode may be used according to standard gene therapy protocols, to treat diseases associated with inappropriate TANGO expression by supplementing a CC patients own production of the polypeptide of to rectify mutations that CC may result in expression of an abnormally active polypeptide. The CC polypeptides may also be used to identify and produce agonists and CC modulate TANGO expression and activity which may be used to complete the polypeptides are CC particularly useful for use as antigens for producing antibodies are CC proteins. They may also be used to detect and quantify the presence of TANGO proteins which may be used for inhibiting the activity of TANGO proteins in samples and therefore identify patients in whom the CC TANGO protein described in the method of the invention.
                    AAA39975
                                   RESULT 13
                                                                                                                                                   Matches
                                                                                                                                                                    Query Match
Best Local
                                                                                    . 1312
AAA39975 standard; cDNA; 2490 BP
                                                                                                                                                                                                                            Sequence 2418 BP; 631 A; 528 C; 594 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This invention describes novel human and murine nucleic acids encoding TANGO polypeptides (which are either wholly secreted or transmembrane proteins) which can be used for gene therapy and/or vaccination. The peptides are designated TANGO 180 to TANGO 189 and TANGO 215. The nucleic acids may be used to produce TANGO 180 to TANGO 189 and TANGO 215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Disclosure;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Isolated nucleic acids encoding TANGO polypeptides useful for preventing, diagnosing and treating diseases associated with inappropriate protein expression -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              P-PSDB; AAY88299
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02-OCT-1998;
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                                                                                                                                                                Local
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                                                                                                                                                 Conservative
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98US-0164169
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                                                                                                                                                               62.5%;
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                                                                                                                                                0;
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Pred. No.
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AAA39975

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15

Query Match Best Local S Matches 15

Similarity

62.5%; Score 15; 100.0%; Pred. No.

ore 15; DB; red. No. 15; Mismatches

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Indels

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Gaps

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21;

Length 2490;

15;

Conservative

0;

Sequence

2490

BP;

642 A;

548 C;

626 G;

669

T; 5

other,

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polypeptides according to standard recombinant DNA methodologies. They may also be used to detect and quantify the presence of TANGO nucleic acids in a sample and therefore identify or dispasse diseases associated with inappropriate TANGO expression (e.g. diseases related to over or under expression of the polypeptides or the expression of inactive polypeptides). The nucleic acids and the polypeptides they encode may be used according to standard gene therapy protocols, to treat diseases associated with inappropriate TANGO expression by supplementing a patients own production of the polypeptide of to rectify mutations that may result in expression of an abnormally active polypeptide. The polypeptides may also be used to identify and produce agonists and antagonists of TANGO expression and activity which may be used to
                            modulate TANGO related processes and diseases. The polypeptides are particularly useful for use as antigens for producing antibodies to TANGO proteins which may be used for inhibiting the activity of TANGO proteins. They may also be used to detect and quantify the presence of TANGO proteins in samples and therefore identify patients in whom the protein is over- or under-expressed. This sequence encodes the human TANGO 187-1 protein described in the method of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                               This invention describes novel human and murine nucleic acids encoding TANGO polypeptides (which are either wholly secreted or transmembrane proteins) which can be used for gene therapy and/or vaccination. The peptides are designated TANGO 180 to TANGO 189 and TANGO 215. The nucle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TANGO 186; TANGO 188; TANGO 189; TANGO 215; TANGO 187; secreted protein; transmembrane protein; gene therapy; diagnosis; treatment; detection; ss.
                                                                                                                                                                                                                                                                                                                                                                                                   acids may be used to produce TANGO 180 to TANGO 189 and TANGO 215 polypeptides according to standard concentration.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Disclosure; Fig 46; 249pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Isolated nucleic acids encoding TANGO polypeptides useful for preventing, diagnosing and treating diseases associated with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2000-293144/25.
P-PSDB; AAY88295.
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02-OCT-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           inappropriate protein expression -
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98US-0164169
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386..1240
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1384 tcagatttattttgg 1398

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This invention describes novel human and murine nucleic acids encoding CC TANGO polypeptides (which are either wholly secreted or transmembrane CC proteins) which can be used for gene therapy and/or vaccination. The CC peptides are designated TANGO 180 to TANGO 189 and TANGO 215. The nucleic acids may be used to produce TANGO 180 to TANGO 189 and TANGO 215. They CC may also be used to detect and quantify the presence of TANGO nucleic acids in a sample and therefore identify or diagnose diseases associated with inappropriate TANGO expression (e.g. diseases related to over or cc under expression of the polypeptides or the expression of inactive used according to standard gene therapy protocols, to treat diseases associated with inappropriate TANGO expression by supplementing a cc used according to standard gene therapy protocols, to treat diseases associated with inappropriate TANGO expression by supplementing a conjugation of the polypeptide of to rectify mutations that a conjugate the protocols are conjugated and the polypeptide of to rectify mutations that a conjugate to standard gene therapy protocols. The protocols are conjugated according to standard gene therapy protocols. The conjugated with inappropriate TANGO expression by supplementing a conjugated to patients own production of the polypeptide of to rectify mutations that a conjugate to the polypeptide of the polypeptide. The conjugate to the polypeptide of the polypeptide and produce agonists and conjugate to the polypeptide of the polypeptide. The conjugate to the polypeptide of the polypeptide and produce agonists and conjugate to the polypeptide of the polypeptide of the polypeptide of the polypeptide of the polypeptide are the polypeptide. The conjugate to the polypeptide of the polypeptide of the polypeptide are the polypeptide of the polype
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TANGO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Isolated nucleic acids encoding TANGO polypeptides useful for preventing, diagnosing and treating diseases associated with inappropriate protein expression -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          P-PSDB; AAY88298
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02-OCT-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TANGO 187-1/2 cDNA.
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98US-0164169
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human; murine;
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BP; 650 A; 557 C; 632 G; 679 T; 5 other;

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AAA39980
This invention describes novel human and murine nucleic acids encoding CC TANGO polypeptides (which are either wholly secreted or transmembrane CC proteins) which can be used for gene therapy and/or vaccination. The CC peptides are designated TANGO 180 to TANGO 189 and TANGO 215. The nucleic CC acids may be used to produce TANGO 180 to TANGO 189 and TANGO 215 CC polypeptides according to standard recombinant DNA methodologies. They CC may also be used to detect and quantify the presence of TANGO nucleic CC with inappropriate TANGO expression of the polypeptides or the expression of inactive CC under expression of the polypeptides or the expression of inactive CC used according to standard gene therapy protocols, to treat diseases CC associated with inappropriate TANGO expression by supplementing a CC may result in expression of the polypeptide of to rectify mutations that CC may result in expression of an abnormally active polypeptide. The CC may result in expression of an abnormally active polypeptide. The CC may result in expression of an abnormally active polypeptide. The CC may result in expression of an abnormally active polypeptides and CC may result in expression of an abnormally active polypeptides and CC may result in expression of an abnormally active polypeptides and CC antagonists of TANGO expression and activity which may be used to CC modulate TANGO related processes and diseases. The polypeptides are
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Matches 15
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1417 tcagatttattttgg 1431
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                                                                                                                                                                                                                                                                                                                                                                                                    Isolated nucleic acids encoding TANGO polypeptides useful for preventing, diagnosing and treating diseases associated with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  P-PSDB; AAY88300.
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02-OCT-1998;
                                                                                                                                                                                                                                                                                                                                                                                          inappropriate protein expression -
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Pred. No.
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Result
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Perfect score:
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Copyright (c) 1993 - 2000 Compugen Ltd
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/cgn2_6/ptodata/2/ina/5B_COMB.seq:*
/cgn2_6/ptodata/2/ina/6A_COMB.seq:*
/cgn2_6/ptodata/2/ina/6B_COMB.seq:*
/cgn2_6/ptodata/2/ina/BCTUS_COMB.seq:*
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US-08-851-968-2
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US-08-9315-793-51
US-09-315-793-51
US-07-638-431-1
PCT-US92-00018-1
US-08-413-13pa-3
US-08-613-13pa-3
US-08-613-13pa-3
US-08-613-13pa-3
US-08-613-13pa-3
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US-09-100-664A-1
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US-09-132-465-4
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US-09-134-918-8
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rddrenne 40' Vidi	5	Sequence 4, Appli	40,	Sequence 5, Appli	Sequence 5, Appli	ω	Sequence 1, Appli		_	,-	16,	80,	Sequence 3, Appli	Sequence 3, Appli	Sequence 1, Appli	Sequence 13, Appl	J,	Sequence 5, Appli

ALIGNMENTS

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Sequence 11 Patent No.
                                                                                                                                                                                                                     PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/10627
FILING DATE: AUGUST 25, 1995
ATTORNEY/AGENT INFORMATION:
NAME: CHRISTENBURY, LYNNE M.
REGISTRATION NUMBER: 30,971
REFERENCE/DOCKET NUMBER: CR-9567-A
                                                                                                                                               TELEFAX: 302-773-0164
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
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TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: DISKETTE, 3.50 INCH
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: MICROSOFT WINDOWS 95
SOFTWARE: MICROSOFT WORD VERSION 7.0A
CURRENT APPLICATION DATA:
MOLECULE TYPE: DI
HYPOTHETICAL: NO
ANTI-SENSE: NO
                                                                                                                                                                     TELECOMMUNICATION INFORMATION: TELEPHONE: 302-992-5481
TELEFAX: 302-773-0164
                                                                                                                                SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STREET: 1007 MAKKE
CITY: WILMINGTON
STATE: DELAWARE
COUNTRY: USA
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                                                                    TYPE: nucleic
STRANDEDNESS:
                                                        TOPOLOGY: linear
                                                                                         LENGTH: 1303 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                          FILING DATE:
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER:
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1007 MARKET STREET
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                                                                                                                                                                                                                                                                                                                                                TELEFAX: (616) 381-5465 INFORMATION FOR SEQ ID NO: 5:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inches,
                                                                                                                                                                                                                                             ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                          FEATURE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: NAKAMURA, YUSUKE
APPLICANT: : FUJIWARA, YOSI
164 ATTTTGGGCTTCAC 151
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                                                                                                                                                                                                                                                                                                                                                                                        ELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OPERATING SYSTEM: MS-DOS 5
SOFTWARE: WordPerfect 5.0
                                                                                                                                       IDENTIFICATION METHOD: experimental examination
                                                                                                                                                             LOCATION:
                                                                                                                                                                                                      LIBRARY:
                                                                                                                                                                                                                                                                            TOPOLOGY:
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                                                                                                                                                                                                                                                                                                                                                                           TELEPHONE:
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                9 attttgggcttcac 22
                                                                                                                                                                         NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                       REFERENCE/DOCKET NUMBER:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US/08/506,864A
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                                                                                                                                                                                                                                                                                                                                                                                                                  Terryence F. Chapman RATION NUMBER: 32549
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FUJIWARA, YOSHIYUKI
WIION: PRLTS PROTEINS AND DNA'S
WIION: ENCODING THE SAME
                                                                                                                                                                                                                                                          genomic DNA
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                                                                   Score 14; ; Pred. No.
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Pred. No.
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                                                                               DB 2; Length 486;
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3.5;
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RESULT 4 US-09-484-345-10

Sequence 10,

Application US/09484345

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Patent No.

NO. 6159734 INFORMATION:

APPLICANT: Robert McKay
APPLICANT: Alexander H. Borchers
APPLICANT: Brenda F. Baker

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US-08-851-968-5/c
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Best Local Similarity
Matches 14; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ZIP: 49008-10-2008
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inches,
MEDIUM TYPE: IBM PC/XT/AT Compatible
COMPUTER: IBM PC/XT/AT Compatible
COMPUTER: SYSTEM: MS-DOS 5.0
                                                                                                                                                                                                                                                                                                                                                                                      TELEPHONE: (616) 381-1156
                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: . JP6-178131 FILING DATE: 29-JULY-1994 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: WordPerfect 5.0 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                      ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION DATA: APPLICATION NUMBER:
                                                                                                                                                                                                                                                                     MOLECULE TYPE:
164 ATTTTGGGCTTCAC 151
                                                                                                                                                                                                                       MMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              UMBER OF SEQUENCES:
                                                                                                                                              LOCATION: 74..371
IDENTIFICATION METHOD:
                                                                                                                                                                           NAME/KEY: exon 3
                                                                                                                                                                                                                                      ORGANISM:
                                                                                                                                                                                                                                                                                                                                                                                                                  REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE:
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                                                                                                                                                                                                                                                                                               STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Terryence F. Chapman
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CITY: Kalamazoo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STREET:
                           9 attttgggcttcac 22
                                                                                                                                                                                                                                                                                                                             ENGTH:
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                                                                                                                                                                                                                                                                                                             nucleic acid
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                                                         Conservative
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                                                                                                                                                                                                      human DNA cosmid library
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                                                                                                                                                                                                                                     Homo sapiens
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                                                                                                                                                                                                                                                                  genomic DNA
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                                                                       58.3%;
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                                                                                                                                              experimental examination
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                                                                       Score 14; pred. No.
                                                         0;
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                                                       Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1.44 Mb storage
                                                                                   DB 2;
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SEQ ID NO 10

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US-08-506-864A-2/c
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; NAME/KEY: CDS
; LOCATION: (859)...(940)
US-09-484-345-10
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Best Local Similarity
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Patent No. 5834245
                                                                                                                                                                INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION NUMBER: US/09/484,345
CURRENT FILING DATE: 2000-01-18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILE REFERENCE: RTS-0104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                   REFERENCE/DOCKET NUMBER: Furuya Case 1334
TELECOMMUNICATION INFORMATION:
TELEPHONE: (616) 381-1156
                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: IBM PC/XT/AT Compatible
COMPUTER: IBM PC/XT/AT Compatible
                                                                   MOLECULE TYPE:
ORIGINAL SOURCE:
ORGANISM: Hom
                                                                                                                                                                                                                                                                                                                  CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: WordPerfect 5.0 CURRENT APPLICATION DATA:
                                                         IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                        ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES:
                                                                                                                      STRANDEDNESS:
                                                                                                                                      TYPE: nucleic acid
                                                                                                                                                                                                                                                   REGISTRATION NUMBER:
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                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER:
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                                                                                            CDNA to mRNA
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381-5465

NO: 2:
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PRLTS PROTEINS AND DNA'S
ENCODING THE SAME
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Pred. No.
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  Query Match 58.3
Best Local Similarity 100.
Matches 14; Conservative
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Sequence 2, App...
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NFORMATION FOR SEQ ID NO:
                                                                                                                                FEATURE
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                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
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APPLICATION NUMBER: JP6-:
FILING DATE: 29-JULY-1990
ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: WordPerfect 5.0 CURRENT APPLICATION DATA:
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                                                                                                                                                         IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                      TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS
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                                                                                                  NAME/KEY:
LOCATION:
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                                                                                     IDENTIFICATION METHOD:
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IDENTIFICATION METHOD:
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62..1189
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58.3%; 5c.
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                 Score 14;
Pred. No
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Pred. No.
    Mismatches
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                            Length 1502;
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Matches

Sequence

APPLICANT:

COUNTRY:

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                        GENERAL INFORMATION:
APPLICANT: Roberts, C
TITLE OF INVENTION: E
TITLE OF INVENTION: E
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Best Local Similarity 100.
14; Conservative
                                                                                                                                                                Sequence 51, Application US/09315793 Patent No. 6221597
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1478 TCAGATTTATTTTG 1465
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ORIGINAL SOURCE:
ORGANISM: Caenorhabditis elegans
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CLONE: SPE-4
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LENGTH: 2539 base pairs
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REFERENCE/DOCKET NUMBER: 60
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATTORNEY/AGENT INFORMATION: NAME: Ferber, Donna M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION DATA:
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| 207 ATTTTGGGCTTCAC 194
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PENTION: SPE-4 RELATED PEPTIDES, ANTIBODIES AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          not relevant
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Christopher J.

ESSENTIAL GENES OF YEAST AS TARGETS FOR ANTIFUNGAL
AGENTS, HERBICIDES, INSECTICIDES AND ANTI-PROLIFERATION
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100.0%; Pred. No
tive 0; Mismat
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Best Local S
Matches 14
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CURRENT FILING DATE: 1999-05-21
NUMBER OF SEQ ID NOS: 62
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 51
LENGTH: 3282
TYPE: DNA
CTENETIC DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Patent No.
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                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                          ORIGINAL SOURCE:
ORGANISM: Plasm
STRAIN: 17X(NL)
                                                                                                                                                                                                                                                            NAME: Spevack, Avrom D. TELECOMMUNICATION INFORMATION: TELEPHONE: (301) 295-6759
                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: PatentIn Release #1.24
CURRENT APPLICATION DATA:
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                                                                                                        HYPOTHETICAL:
ANTI-SENSE: N
                                                                                                                                    MOLECULE TYPE:
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MMEDIATE SOURCE
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                           DEVELOPMENTAL STAGE: TISSUE TYPE: Blood
                                                                                                                                                       TOPOLOGY:
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NMRDC Building 1 T-12 National Naval
Medical Center
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Hedstrom, Richard
Khusmith, Srisin
                                                                         Plasmodium yoelii
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             erythrocytic stage
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                                        erythrocytic stage
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; OTHER INFORMATION:
US-07-638-431-1
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Best Local Similarity
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                                                                                                                                                  HYPOTHETICAL: N
ANTI-SENSE: N
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                 TELEFAX: (301) 295-40
NFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                          NAME: Spevack, Avram D. TELECOMMUNICATION INFORMATION: TELEPHONE: (301) 295-6759
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NAME: Spevack, Avram D.
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                             FEATURE:
                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS:
LENGTH: 4673 base pairs
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                                                                    MMEDIATE SOURCE:
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                                                                TISSUE TYPE: Blood
TOTAL TYPE: erythrocytic stage
                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: IBM PC
OPERATING SYSTEM:
SOFTWARE: Patenti
NAME/KEY:
LOCATION:
                                                                                                                         ORGANISM: Plasm
STRAIN: 17X(NL)
                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: PCT/US92/00018
FILING DATE: 19920103
CLASSIFICATION: 424
                                                                                              TISSUE TYPE: Blood
                                                      LIBRARY:
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                                                                                                                                                                                                                                      TYPE: NUCLEIC ACID
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LOCATION: 718..3195
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                                     (: Py-lambdagt11-2-7 kb genomic expression
Py10.1111
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Py10.1111
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                USA
                                                                                                                                      Plasmodium yoelii
                                                                                                                                                                                        linear.
E: DNA (genomic)
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Khusmith, Srisin
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                                                                                                            erythrocytic stage
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US-08-488-271B-33/c
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  Sequence 33, Application US/08488271B Patent No. 5892013
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US-08-479-275D-33
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                                                    Query Match
Best Local Similarity
Matches 13; Conserv
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Best Local Similarity 100.0%;
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                                                                                                                                 TOPOLOGY: 1: MOLECULE TYPE:
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                                                                                                                                                                                                                                                                                           CLASSIFICATION: 510
ATTORNEY/AGENT INFORMATION:
NAME: Lambiris, Elias J.
                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
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            11 tttgggcttcact 23
14 TITGGGCTTCACT
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                                                                                                                                                                                                                                                                                                                                                                        COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
                                                                                                                                                           STRANDEDNESS:
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                                                    Conservative
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Thellersen, Marianne
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Ib G
                                                              54.2%; Score 13; 100.0%; Pred. No.
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Pred. No.
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                                                   Mismatches
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                                                                         Length 23;
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                                                 Indels
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(PPLICANT:

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US-08-631-319A-3
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                                                                                                                                                                                                                                                                                                                Sequence 3, Application US/08631319A Patent No. 6117641
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       INFORMATION FOR SEQ ID NO:
COMPUTER READABLE FORM:
MEDIOM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII (text)
                                                                                                                                                                                                                                                   APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEPHONE: 212-867-0123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS
                                                                                                                                                                                                             TITLE OF INVENTION: Assay and Reage TITLE OF INVENTION: Fungal Agents,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                 UMBER OF SEQUENCES:
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REGISTRATION NUMBER: 33,
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US/08 FILING DATE: 07-JUNE-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                       COUNTRY: UZIP: 02109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION:
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                                                                                                                                                                    ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: PatentIn Release #1.0, Version #1.25
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                                                                                                                                   Boston
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                                                                                                      USA

    No. 5892013o No. 5892013disk of No. 5892013th America,
    Lexington Avenue, Suite 6400

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Ohya, Yoshikazu
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                                                                                                                                                                 FOLEY,
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Fungal Agents, and Uses Related Thereto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        54.2%; Score 13; 100.0%; Pred. No.
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US-08-842-306B-17
Sequence 17, Application US/08842306B; Patent No. 6271197
GENERAL INFORMATION:
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Best Local Similarity
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 832-1000
TELEFAX: (617) 832-7000
INFORMATION FOR SEQ ID NO: 3:
INFORMATION FOR SEQ ID NO: 17
SEQUENCE CHARACTERISTICS
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NAME: Pham, Chinh H.
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                                                                                                                                        APPLICATION NUMBER: US 08/771,212
ETILING DATE: 20-DEC-1996
APPLICATION NUMBER: US 08/631,319
ETILING DATE: 11-APR-1996
ATTORNEY/ACENT INFORMATION:
                                                                                                                                                                                                                                                               CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/842,306B
                                                                                                                                                                                                                                                                                                                                                          ZIP: 02109-2170
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                   TELECOMMUNICATION INFORMATION: TELEPHONE: 617-832-1000
                                                                                                                                                                                                                                     FILING DATE: 23-Apr-1997 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS:
ADDRESSEE: FOLEY,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Berlin, Vivian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       : 42 base pairs
                                                                                     NAME: Vincent, Matthew P.
REGISTRATION NUMBER: 36,709
REFERENCE/DOCKET NUMBER: MIV-074.04
                                                                                                                                                                                                                                                                                                         COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: WordPad
                                                                                                                                                                                                                                                                                                                                                                                                                                        STATE: MA
                                                                                                                                                                                                                                                                                                                                                                                                                                                     CITY: Boston
                                    TELEFAX: 617-832-7000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Levin, David
Ohya, Yoshikazu
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-832-1000
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 42 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
DESCRIPTION: /desc = "primer"
SEQUENCE DESCRIPTION: SEQ ID NO: 15:
US-08-838-973B-15
                         Query Match
Best Local Similarity 100.0
Watches 13; Conservative
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TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear.
MOLECULE TYPE: other nucleic acid
DESCRIPTION: /desc = "primer"
SEQUENCE DESCRIPTION: SEQ ID NO: 17:
US-08-842-306B-17
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GENERAL INFORMATION:
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Best Local Similarity 100
Matches 13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: IBM PC COMPACTIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOPTWARE: Patentin Release #1.0, Version #1.30
CURREWT APPLICATION DATA:
APPLICATION NUMBER: US/08/838,973B
FILING DATE: 23-Apr-1997
PRIOR APPLICATION NUMBER: US 08/631,319
APPLICATION NUMBER: US 08/631,319
FILING DATE: 10-APR-1996
AFTORNEY/AGENT INFORMATION:
NAME: Vincent, Matthew P.
REFERENCE/DOCKET NUMBER: 36,709
REGISTRATION NUMBER: 36,709
REFERENCE/DOCKET NUMBER: MIV-074.05
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ZIP: 02109-2170
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
ADDRESSEE: FOLEY, HOAG & ELIOT LLP
STREET: One Post Office Square
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Berlin, Vivian
Damagnez, Veronique
Smith, Susan
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION: ASSAYS AND REAGENTS FOR IDENTIFYING ANTI-FUNGAL AGENTS, AND USES RELATED THERETO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CITY: Boston
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/ 100.0%; Pr
                                                  54.2%; Score 13; DB 4; Length 42; 100.0%; Pred. No. 43; ative 0; Mismatches 0; Indels
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Pred. No.
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Db 30 CAGATTTATTTTG 42

Search completed: November 15, 2001, 05:55:52 Job time: 6743 sec

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Title: .
Perfect score:
Sequence:
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Maximum DB seq length: 200000000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Word size
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Searched:
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Gapop 60.0 , Gapext 60.0
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Copyright (c) 1993 - 2000 Compugen Ltd
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gb_est20:*
gb_est21:*
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gb_est2:*
gb_est3:*
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gb_est37:*
gb_est38:*
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gb_est34:*
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gb_est24:*
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gb_est17:*
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gb_est12:*
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em_esthum5:*
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em_estrol1:*
em_estrol2:*
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em_estpl9:*
em_estpl10:*
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em_estpl5:*
em_estpl6:*
em_estpl7:*
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em_estpl1:*
em_estpl2:*
em_estpl3:*
                                                                                     gb_est28:*
gb_est29:*
gb_est30:*
gb_est31:*
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gb_est25:*
gb_est26:*
gb_est27:*
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em_estro18:*
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em_esthum16:*
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gb_est42:*
gb_est43:*
gb_est44:*
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gb_est46:*
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em_estro7:*
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em_estro3:*
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gb_est41:*
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em_estin3: *
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em_esthum25:*
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gb_est52: *
gb_est53: *
gb_est54: *
gb_est55: *
gb_est56: *
gb_est57: *

gb_est48:*
gb_est49:*
gb_est50:*
gb_est51:*

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em_gss_rod8:*
gb_gss35:*
gb_gss36:*
gb_gss37:*
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gb_gss29:*
gb_gss30:*
gb_gss31:*
gb_gss31:*
gb_gss33:*
gb_gss34:*
                                          em_gss_inv4:*
em_gss_rod6:*
em_gss_rod7:*
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em_gss_pln1:*
em_gss_pln2:*
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em_gss_rod2: *
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em_gss_hum9:*
em_gss_inv1:*
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gb_gss27:*
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em_gss_hum6:*
em_gss_hum7:*
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gb_est111:*
gb_htc:*
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gb_gss16:*
gb_gss17:*
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gb_gss13:*
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gb_est90:*
gb_est99:*

gb_est89: gb_est88:* gb_est87: gb_est85: gb_est84: gb_est83: gb_est82: gb_est81: gb_est80:

gb_est86:

gb_est102: gb_est100:

gb_est103:

gb_est76: gb_est77:

gb_est66:

gb_est65:* gb_est64: gb_est62:* gb_est61: gb_est59:

gb_est63:

gb_est60: gb_est58:*

gb_est78:*
gb_est79:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

gb_est95:*
gb_est96:*
gb_est97:*
gb_est98:*
em_esthum29:*
em_esthum30:*

gb_est107:*
gb_est108:*
gb_est109:*

em_estro22:*
em_estro23:*
em_htc:*

em_esthum32:*
em_esthum33:*
em_estom3:*

em_estpl11:*
em_estro21:*

gb_est72: gb_est73: gb_est74: gb_est91: gb_est92: gb_est93: gb_est94:

gb_est70:* gb_est71:* gb_est69: gb_est67: gb_est106:* gb_est105:

2030 E.,

, OJS

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SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                            RESULT 1
A2422893/c
                                                                                                REFERENCE
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                                                                                                                                                                                                                    VERSION
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No.
                                                                              AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score
            Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Rei,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern and Wright,D.,Welss,R.
                                                                                      Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae;
1 (bases 1 to 426)
                                                                                                                                                                                                                                    AZ422893 426 bp DNA GSS 03-OCT-2000 IM0201G13R Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0201G13 R, DNA sequence.
                                                                                                                                                                                              GSS.
                                                                                                                                                                          house mouse
                                                                                                                                                                                                                AZ422893.1
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BG442137
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AI915011
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AZ856834
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AQ40938
AQ440938
AQ547803
AQ547803
AU085116
AU045115
AU0453320
AQ5486320
AZ5486748
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AZ5183973
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                                                                                                            Muridae;
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AA077273 7B11G05 C
A1079841 ox50d02.x
A1040896 A0040896
AU017418 AU017418
AU045114 AU045114
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AW528260 U1-R-BT1-
AQ705173 HS_5520_B
AA528604 nf02c09.s
AQ237895 RPCI11-68
AI914472 wd49e06.x
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A2609907 1M0434122
BG442137 GA_Ea001
BB566737 BB566737
A1915011 tq97b12.x
BB149447 BB149447
D79868 HUM345A06B
BB354670 BB354670
                              Niederhausern, A.
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AZ609907 1M0434I2;
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AQ225246 HS_2012_B
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Anopheles
EST276425
AU180439
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1 2M0161H20
2 SP_1003_A
601101687
2 AF010852
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RPCI-11-3
AU085116
AU045115
AU023320
RPCI-11-3
SP_1002_A
RPCI-23-4
                                                  Reilly
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    REFERENCE
AUTHORS
TITLE
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AW528260
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                                                                                                                          ORGANISM
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                                                                                                                                                                                                                                                                                                                                                      source
                                                                        Norway rat.
Rattus norvegicus
Eukaryota; Metazoa; C
Mammalia; Eutheria; F
                                                                                                                                                                                                          AW528260 406 bp mRNA EST 06-MAR-2000 UI-R-BT1-ajw-e-04-0-UI.S1 UI-R-BT1 Rattus norvegicus cDNA clone UI-R-BT1-ajw-e-04-0-UI 3', mRNA sequence.
                        1 (bases 1 to 406)
Bonaldo, M.F., Lenno
Normalization and subtraction: two approaches
                                                              Rattus.
                                                                                                                                                                EST
                                                                                                                                                                                AW528260.1
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Class: plasmid ends
High quality sequence stop: 426
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Erro
Plate: 0201 row: G column: 1
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Tel: 801 585 5606
Fax: 801 585 7177
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                University of Utah
University of Utah
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Seq primer: CACACAGGAAACAGCTATGACC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       130
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                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with 74 DNA polymerase and 74 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gil4732114|gb\AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coll XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
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/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (http://www.jax.org/resources/documents/dnares/).
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/clone="UUGC1M0201G13"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
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/strain="C57BL/6J"
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100.0%; Pr
100.0%; O;
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                      Lennon, G. and Soares, M.B
                                                                        Chordata; Craniata; Vertebrata; Euteleostomi; Rodentia; Sciurognathi; Muridae; Murinae;
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                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 591)

Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T., Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D. a
                                                                                                                                                                                                                  AQ705173 591 bp DNA
HS_5520_B1_E02_T7A RPCI-11 Huma
genomic clone Plate=1096 Col=3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 strand cDNA and therefore this may represent a bonafide poly A tail. The sequence tag present in the cDNA between the NotI site and the oligo-dT track served to identify it as a clone from the normalized corpus-striatum library cDNA Library Preparation: M.B. Soares Lab Clone distribution: clones will be available through Research Genetics (www.resgen.com) The following repetitive elements were found in this cDNA sequence: 1-29, >AT_richtLow_complexity 64-178, >RSINEI#SINE/BA(B5)
Hood, L.
                                                                                                                                                                  GSS
                                                                                                                                                                                    AQ705173.1
                                                                                                                     Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The sequence contained an oligo-dT track that was present in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Email: msoares@blue.weeg.uiowa.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              University of Iowa
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note-"Vector: pT/T3D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; The library UI-R-BT1 is a subtracted library derived from a mixture of the following tissues: hippocampus, thalamus, mid-brain, medulla, corpus striatum, cerebral cortex and testis. For
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TAG_LIB-UI-R-BT1
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6:791–806, 1996)
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FAG_SEQ=CTAGG*
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/clone_lib="UI-R-BT1"
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/db_xref="taxon:10116"
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                                                                                                                                                                                  GI:5414599
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                                                                                                                                                                                                                                                                                       Contact: Robert Strausberg, Ph.D. Email: cgapbs-r@mail.nih.gov
                                                                                                                                                                                                                         Tissue Procurement: L. Jeffrey Medeiros, M.D., Michael Emmert-Buck, M.D., Ph.D.
                                                                                                                                                                                                                                                                                                                                                                     Unpublished (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

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National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens
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Clones are derived from the human BAC library RPCI-11. For BAC
Library availability, please contact Pieter de Jong
(pieter@dejong.med.buffalo.edu). Clones may be purchased from
BACPAC Resources (http://bacpac.med.buffalo.edu/ordering.bac.htm)
or from Resear h Genetics (info@resgen.com). BAC end Web Server:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    High quality sequence stop: 591.
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(206) 616-3887
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          and party.
ECORI Methylase. Size Server
pBACe3.6 vector at ECORI sites"
137 c 103 g 216 t
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Male blood DNA was isolated
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /clone_lib="RPCI-11 Human Male BAC Library"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /db_xref="taxon:9606"
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Pred. No.
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33;
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                                                                     Genome Sequencing Center thution information can be
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BASE COUNT
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Best Local :
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                                                                                                                                                                                                                                                                                                                   Email: mdadams@tigr.org
Clones are derived from the human BAC library RPCI-11. For BAC
Clones are darived from the human BAC library RPCI-11. For BAC
Clones are darilability, please contact Pieter de Jong
(pieter@dejong.med.buffalo.edu). Clones may be purchased from
BACPAC Resources (http://bacpac.med.buffalo.edu/ordering) or from
Research Genetics (int@resgen.com). BAC end search page:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Contact: Mark Adams
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville,
                                                                                                                                                                                                                                                                                                      http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Other_GSSs: RPCI11-68J13.TJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Adams, M.D., Rounsley, S.D., Zhao, S., Bass, S., Linher, K., Golden, K., Berry, K., Granger, D., Suh, E., Wible, C., de Jong, P. and Venter, J.C. Use of human BAC End Sequences for Sequence-Ready Map Building
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AQ237895 210 bp DNA GSS Clone PCII1-68J13.TK RPCI-11 Homo sapiens genomic clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Unpublished (1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens
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301 838 0208
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        /Cell_type="Lymphocytes"
/note="Vector: pBACe3.6; Site_1: EcoRI; Site_2:
RPCIII Human Male BAC Library"
20 c .32 g 71 t 2 others
                                                                                                                                          /organism="Homo sapiens"
/db_xref="GDB:7525956"
/db_xref="taxon:9606"
/clone="RPCI-11-68J13"
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27 c 23 g 56 t
                                                                                                                           /clone_lib="RPCI-11"
                                                                                                                                                                                                                                                  ocation/Qualifiers
                                                                                                        'sex≖"Male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eutheria;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:912592"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /tissue_type="kidney"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /clone_lib-"NCI_CGAP_Kid1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ocation/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Chordata; Craniata; Vertebrata; Euteleostomi; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MD 20850, USA
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                                                                   RESULT
BB528140
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AUTHORS
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SOURCE
                                  DEFINITION
                                                        Locus
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Best Local S
Matches 16
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                          BB528140
BB528140
                                                                                                                                                                                                                                          l Similarity
16; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A1914472 266 bp mRNA EST 17-DEC-1 wd49e06.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2331490 3' similar to 9b:X63547_cds2 UBIQUITIN CARBOXYL-TERMINAL HYDROLASE TRE-2 (HUMAN);, mRNA sequence. A1914472
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Tumor Gene Index
Unpublished (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 266)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                          /note-*Organ: pooled; Vector: pT773D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; Equal amounts of plasmid DNA from three normalized libraries (fetal lung NbHL19W, testis NHT, and B-cell NCI_CGAP_GCB1) were mixed, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from pools of 5,000 clones made from the same 3 libraries. The pools consisted of I.M.A.G.E. clones 297480-302087, 682632-687239, 726408-728711, and 729096-731399. Subtraction by Bento Soares and M. Fatima Bonaldo. **
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268 bp mRNA EST 28-JUL-2000 RIKEN full-length enriched, 15 days embryo head Mus cDNA clone D930045A20 3', mRNA sequence.
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/db_xref="taxon:9606"
/clone="IMAGE:2331490"
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/lab_host="DH10B"
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1.1e+02;
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VERSION KEYWORDS

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Thermostabilization and thermoactivation of thermolabile enzymes by trehalose and its application for the synthesis of full length cDNA. Proc. Natl. Acad. Sci. U.S.A. 95 (2), 520-524 (1998)
Itoh,M., Kitsunai,T., Akiyama,J., Shibata,K., Izawa,M., Kawai,J., Tomaru,Y., Carninci,P., Shibata,Y., Ozawa,Y., Muramatsu,M., Okazaki,Y., Muramatsu,M., Okazaki,M., Okazaki,M., Muramatsu,M., Okazaki,M., Mura
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URL:http://genome.rtc.riken.go.jp/
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3-1-1 Koyadai, Tsukuba, Ibaraki 305-0074, Japan
Tel: +81-298-36-9013
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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                                                                                                                  prepared by using trehalose thermo-activated reverse transcriptase and subsequently enriched for full-length by cap-trapper. Second strand cDNA was prepared with the primer adapter of sequence [5]
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                                                /db_xref="taxon:10090"
/clone="D930045A20"
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/dev_stage="15 days embryo"
/lab_host="DH10B"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Email: genome-res@rtc.riken.go.jp,
URL.http://genome.rtc.riken.go.jp/
Carninci.P., Nishiyama,Y., Westover,A.,
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Tel: +81-298-36-9013
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The Institute of Physical and Chemical Research
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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                                                                                                                                                                                                                                            details
                                                                                                                                                                                                                                                           visit our web site (http://genome.rtc.riken.go.jp) for
                                                                              /organism="Mus musculus"
/db_xref="taxon:10090"
   /clone_lib="RIKEN full-length enriched,
                                                                                                                                                                                                Cocation/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ξK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            64 c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 16; DB 160;
Pred. No. 1.1e+02;
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                                                                                                                                                                     Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                            Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. J
                                                                                                                                                                                                                                                                                                                                    White,Y., Wylie,T., Waterst
                                                                                                                                                                                                                                                                                                                                             Krizman, D., Kucaba, T., Lacy, M., Le, N., Lennon, G., Marra, M., Martin, J., Moore, B., Schellenberg, K., Steptoe, M., Tan, F., Theising, B., White, Y., Wylie, T., Waterston, R. and Wilson, R.
                                                                                                                                                                                                                                                                                                                                                                                           Hillier, L., Allen, M., Bowles, L.,
                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 294)
                                                                                                                                                                                                                                                                                                             Contact: Wilson RK
                                                                                                                                                                                                                                                                                                                          Unpublished (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     zp01g06.rl Stratagene ovarian cancer (#937219) Homo sapiens cDNA clone IMAGE:595162 5', mRNA sequence.
                                                                                                                                                                High quality sequence stop: 260.
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens
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/dev_stage="adult, 64 years"
/lab_host="SOLR (kanamycin resistant)"
/note="Yector: Bluescript SK-; Site_1: EcoRI; Site_2: XhoI
/note="Yector: Bluescript SK-; Primer: Oligo dT. Papillary
                                                                                          /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:595162"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /clone_lib="Stratagene ovarian
                                                                /sex="female"
                                                                                                                                                   Location/Qualifiers
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/dev_stage="12 days em
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Pred. No. 1.1e+02;
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                                                                           cancer (#937219)"
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||||||||||||||
                                                                                                                                                                                                                                                                                                                               Email: egreen@nhgri.nih.gov
Plate: 11 row: G column: 05
Seq primer: -21M13 (ABI).
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                    Genome Technology Branch
National Human Genome Research Institute/NIH
49 Convent Dr., MSC4431, Building 49, Room 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2006 expressed-sequence tags derived from human chr. 7-enriched cDNA libraries Genome Res. 7 (3), 281-292 /1997
                                                                                                                                                                                                                                                                                                                                                                                                           Fax: 3014024735
                                                                                                                                                                                                                                                                                                                                                                                                                             Tel: 3014020201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Contact: Eric D. Green
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Touchman, J.W., Bouffard, G.G., Weintraub, L.A., Idol, J.R., Wang, L., Robbins, C.M., Nussbaum, J.C., Lovett, M. and Green, E.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 295)
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              63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       107
         /sex="female and male mixture"
/tissue_type="brain"
/dev_stage="pool of 9 week and 12 week"
/lab_host="E. coli strain DH5 alpha"
/note="Organ: brain; Vector: pawF10; cDNA was generated from cytoplasmic RNA using a mixture of random DNA hexamers and oligo(dT). From this pool of cDNA, human chromosome 7-enriched cDNA was isolated by direct cDNA selection using chromosome 7 genomic DNA (cosmids). The resulting direct-selected cDNA was cloned into a plasmid vector using a non-directional uracil DNA glycosylase (UDG)-mediated cloning strategy."

63 a 56 c 76 g 93 t 7 others
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                                                                                                                                                                                                                                                         /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="7B11G05"
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ches 0;
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       7 others
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                                  Mus musculus
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
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                                                                                                                 AU040896
                                                                                                                        AU040896 427 bp mRNA
AU040896 Mouse four-cell-embryo
J0820C10 3', mRNA sequence.
                                                                                                                                                                                                                                                              16; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A1079841 337 bp mRNA EST 28-AUG-1998 ox50d02.x1 Soares_total_fetus_Nb2HF8_9w Homo sapiens cDNA clorange:1659747 3', mRNA sequence.
                                                                             house mouse.
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1 (bases 1 to 337)
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National Cancer Institute, Cancer Genome Anat
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(bases 1 to 427)

M.S.H., Kitchen, J.R., Wang, X., Threat, T.A., Sun, T., D.

Liang, Y., Kargul, G.J., Sharara, R., Lim, M.K. and Doi, H.
                                                                                                                                                                                                                                                                                                                                     119
                                                                                                                                                                                                                                                             Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /clone_lib="Soares_total_fetus_Nb2HF8_9w"
/dev_stage="8-9 weeks"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /clone="IMAGE:1659747"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                                                    GI:3954720
                                                                                                                                                                                                                                                                       66.7%;
                                                                                                                                                                                                               51
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                                                                                                                                                                                                                                                           0;
                                                                                                                                                                                                                                                                       Score 16;
Pred. No.
                                                                                                                                                                                                                                                           Mismatches
                                    Craniata; Vert
Sciurognathi;
                                                                                                                                     cDNA Mus musculus
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hes 0;
                                                                                                                                                                                                                                                                                 DB 15;
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                                                 Vertebrata; Euteleostomi;
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                                                                                                                                                                                                                                                                                Length 337;
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                                      Muridae;
             Sun, T., DePalma, G.E
                                                                                                                                    cDNA clone
                                    Murinae;
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TTATTTTGGGCTTCAC 405
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                                                                                                          16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Unpublished (1998)
Contact: Hirofumi Doi
Doi Bloasymmetry Project, ERATO
Japan Science and Technology Corporation (JST)
WBG Marive East 12F, 2-6 Nakase, Mihama-ku, Ch.
Email: hd@bloa.jst.go.jp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NO.M.S.H. Kitchen, J.R., Wang, X., Threat, T.A., Sun, T., DePalma, G.E., Liang, Y., Kargul, G.J., Sharara, R. and Doi, H.
Systematic analyses of genes expressed in 2-cell stage mouse embryos (The ERATO/Doi Project at Wayne State University) (Ko., M.S.H. et al.)
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AU017418
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AU017418
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1 (bases 1 to 439)
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mus musculus
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Doi Bloasymmetry Project, ERATO
Japan Science and Technology Corporation (JST)
WBG Marive East 12F, 2-6 Nakase, Mihama-ku, Chiba
Email: hd@bioa.jst.go.jp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Systematic analyses of gene
ERATO/Doi Project at Wayne
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                                                                                                                                                                                                                                                            /db_xref="taxon:10090"
/clone="J0738H04"
/clone_lib="Mouse two-cell stage embryo cDNA"
/dev_stage="two-cell stage embryo"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mouse two-cell stage embryo cDNA Mus musculus 3', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                      /organism-"Mus musculus"
/strain-"C57BL/6J"
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/dev_stage="four-cell-embryo"
62 c 107 g 135 t
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/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="J0820C10"
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                                                                                                    DB 107;
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hes 0;
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thes 0;
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                                                                                                          Indels
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                                                                                                                                                                                                                                                                                                                                                                                                              AA682402 489 bp mRNA EST 19-DEC-1997 z]86d05.s1 Soares_fetal_liver_spleen_lNFLS_S1 Homo sapiens cDNA clone IMAGE:461769 3' similar to gb:M33600 HLA CLASS II HISTOCOMPATIBILITY ANTIGEN, DR-1 BETA CHAIN (HUMAN);, mRNA
                                          4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                      White, Y., Wylie, T., Watersto
WashU-NCI human EST Project
                                                                                                                                                                  Hillier,L., Allen,M., Bowles,L., Dubuque,T., Geisel,G., Jost,S., Krizman,D., Kucaba,T., Lacy,M., Le,N., Lennon,G., Marra,M., Martin,J., Moore,B., Schellenberg,K., Steptoe,M., Tan,F., Theising,B., White,Y., Wylie,T., Waterston,R. and Wilson,R.
                                                                                             Washington University School of Medicine
                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                      AA682402
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Contact: Hirofumi Doi
Doi Bloasymmetry Project, ERATO
Japan Science and Technology Corporation (JST)
WBG Marive East 12F, 2-6 Nakase, Mihama-ku, Chiba 261-71, Japan
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                                                                                                                                        Unpublished (1997)
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KO,M.S.H., Kitchen,J.R., Wang,X., Threat,T.A., Sun,T., DePalma,G.E., Ling,Y., Kargul,G.J., Sharara,R., Lim,M.K. and Doi,H.

Systematic analyses of genes expressed in 16-cell mouse embryo (The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ERATO/Doi Project at Wayne State University)
Unpublished (1998)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Email: hd@bioa.jst.go.jp.
Location/Qualifiers
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{\sf est@watson.wustl.edu} lone is available royalty-free through LLNL ; contact the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3', mRNA sequence.
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/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="J0930C10"
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/dev_stage="sixteen-cell-embryo"
65 c 114 g 140 t
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                                                                                       ORIGIN
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10 TTTATTTTGGGCTTCA 25
                  6 tttattttgggcttca 21
                                                                                                                                                                                                                                                                                                          IMAGE Consortium (info@image.llnl.gov) for further information. Seg primer: -40ml3 fwd. ET from Amersham
                                               Similarity
                                                                                                                                                                                                                                                                                                   High quality sequence stop: 427.
                                                                                               127
                                      Conservative
                                                                                        þ
                                                                                                                                                                                                                                       /clone_lib="Soares_fetal_liver_spleen_lNFLS_S1"
                                                                                                                                                                                                                                 /sex="male"
                                                                                                                                                                                                                                                    /clone="IMAGE:461769"
                                                                                                                                                                                                                                                             /db_xref="taxon:9606"
                                                                                                                                                                                                                                                                        'organism-"Homo sapiens"
                                                                                                                                                                                                                                                                                           ocation/Qualifiers
                                               100.0%;
                                                        66.78;
                                              Score 16; Pred. No.
                                      0
                                     Mismatches
                                                       DB 10;
                                              1.1e+02;
                                                      Length 489;
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Search completed: November 15, 2001, 06:39:15 Job time: 9291 sec

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Minimum DB :
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Copyright (c) 1993 - 2000 Compugen Ltd
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160 161 162 163 164 165 165

156 157

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Result

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Score

Match

Length

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SUMMARIES

AA251974

100.0 100.0 100.0

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AA251974 67 bp mrNA EST 12-MAR-1997 zr64e0l.sl Soares_NhHMPu_Sl Homo sapiens cDNA clone IMAGE:668184 3's similar to gb:D25272 !!!! ALU CLASS A WARNING ENTRY !!!! (HUMAN);
                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 67)
  Elliston, K., Hawkins, M., Holms, Lennon, G., Marra, M., Parsons, Tan, F., Trevaskis, E., Waterst
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N23691 yw46b01.s1
N23691 yw46b01.s1
D82540 HUMHBC4284
N29962 yw53f06.s1
AI433008 th42e09.x
AA484085 ne73c10.s
H67529 yu68c11.s1
AQ53772 RPCI-11-4
AA52838 ne82h04.s
AF149534 AF149534
AI357151 qx62g10.x
AW574959 UT-HF-BNO
AI824449 wc48a05.x
AF196442 tw61e03.x
AA573262 nm52d10.s
BF983577 60230724
AA55272 CTFB1-E1-
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AA091710 m1216.seq
AA091710 m1216.seq
AA047496 oe19a05.s
AW082537 xb52608.x
AA632600 np82c09.s
AA632600 np82c09.s
AA1305894 qw73e10.x
AA668816 ad41d11.s
AA1306191 qw74f02.x
AA1306208 qw74g10.x
B95154 CIT-HSP-217
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AA730009 nz89g05.s
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AA228795 nc14e07.s
AA247810 hfe0642.s
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AA457423 aa86b02.r
AA835205 ak64h01.s
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AUTHORS
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                                                                                                            Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D.,
                                                                                                                                                                                  NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy
Tumor Gene Index
Unpublished (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                            wv46el0.xl
similar to
                                                                                                                                                                                                                                                                                                                                                                     EST
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found through the I.M.A.G.E. Consortium/LLNL at:
            CDNA Library Preparation: Life Technologies, Inc. cDNA Library Arrayed by: Greg Lennon, Ph.D. DNA Sequencing by: Washington University Genome S Clone distribution: WCI-CGAP clone distribution i
                                                                                                     Emmert-Buck, M.D., Ph.D.
                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                          Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                      AW007890.1 GI:5856668
                                                                                                                                                                                                                                                                                                                                                                                                           AW007890
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AW007890
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. Trace considered overall poor quality Seq primer: -41ml3 fwd. ET from Amersham
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Fax: 314 286 1810
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Contact: Wilson RK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The WashU-Merck EST Project
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Email: est@watson.wustl.edu
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note-*Organ: mixed (see below); Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; Equal amounts of plasmid DNA from three normalized libraries (melanocyte 2NbHM, pregnant uterus NbHPU, and fetal heart NbHH19W) were mixed, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from pools of 5,000 clones made from the same 3 libraries. The pools consisted of I.M.A.G.E. clones 260232-265223, 340488-345479, and 484488-489479.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /tissue_type="Pooled human melanocyte,
pregnant uterus"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:668184"
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                                                                                                                                                                                                                                                                                                                                                                                                                   72 bp mRNA EST 09-MAR-2000 NCI_CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2532618 contains Alu repetitive element;, mRNA sequence.
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                                                                                                                                                                                                                                                                                Chordata;
Primates;
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Pred. No. 2.2;
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                                                                                                                  Ph.D.,
              Sequencing Center 
information can be
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SOURCE ORGANISM VERSION KEYWORDS

Homo sapiens

ACCESSION

mRNA sequence. AA251974 AA251974.1 GI:1887144

REFERENCE

AUTHORS

Hillier,L., Clark,N., Dubuque,T., J., M., Hultman,M., Kucaba,T., Le,M., Rifkin,L., Rohlfing,T., Soares,M.,

RESULT 1 AA251974/c

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100.0 100.0 100.0

2 AA826076 20 AW769572 03 AI922803 AA346355

ALIGNMENTS

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100

AA017501 AA091710

AA847496

AW082537 AA632600 AI305894

1000

228

BF983677 AQ427220

AA455670

AA730009

AA573262

AI696442

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1000

218

AF149534

30 AQ553772 AA528383

AA484085

AI433008

D82540

122 122 126 126 128 133

AI357151 8 AW574959 2 AI824649

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100 100 100 100

105 107 107

145 159 159 157

AA247810

BF194862

AA228795 AA604960

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103

AI864984

AA828120

AA457423 AA835205

DEFINITION LOCUS

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AUTHORS
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ORGANISM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   18;
                                                                                                                                                                                                                                                                          Source: IMAGE Consortium, LLNL This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hilller,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M., Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M., Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F., Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and Wilson,R.

The WashU-Merck EST Project
                                                                                                                                                                                                                                                 High quality sequence stop: 253
                                                                                                                                                                                                                                                                    Seq primer: m13 -40 forward
                                                                                                                                                                                                                                                                                                                                                  Email: est@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                   Tel:
                                                                                                                                                                                                                                                                                                                                                                                                           Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Unpublished (1995)
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Hillier,L., Clark,N.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
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YY80hll.s1 Soares_multiple_sclerosis_2NbHMSP Homo sapiens cDNA

clone IMAGE:279909 3' similar to contains Alu repetitive eleme
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: Wilson RK
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Insert Length: 508 Std Error: 0.00
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314 286 1810
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/tissue_type="multiple sclerosis lesions"
/dev_stage="Age 46"
/lab_host="DH10B (ampicillin resistant)"
/note="Vector: pT7T3D (Pharmacia) with a
                                                                                      /clone_lib="Soares_multiple_sclerosis_2NbHMSP"
/sex="male"
                                                                                                                            /db_xref="taxon:9606"
/clone="IMAGE:279909"
                                                                                                                                                                /organism="Homo sapiens"
/db_xref="GDB:3898285"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /clone="IMAGE:2532618"
/clone_lib="NCI_CGAP_Gas4"
/tissue_type="poorly differentiated adenocarcinoma with
signet ring_cell_features"
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/db_xref="taxon:9606"
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  with a modified
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FEATURES
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Best Local S
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h 100.0%; Score 18; Similarity 100.0%; Pred. No. 18; Conservative 0; Mismatcl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              18;
                                                                                                                                                                                                                                                                                              Seq primer: KS
                                                                                                                                                                                                                                                                                                                                     Tel: 2016481008
Fax: 2016481007
Email: rhart@andromeda.rutgers.edu
sequence is similar to complement Cl inhibitor gene (M30688) and
                                                                                                                                                                                                                                                                                                           subcloned into PCRscript
                                                                                                                                                                                                                                                                                                                                  contains alu element
                                                                                                                                                                                                                                                                                                                                                                                                                            Rutgers University
Dept of Biol Sci,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Kuchinke, W., Hart, R.P. and Jonakait, G.M. Identification of mRNAs regulated by interferon-gamma rat astrocytes by PCR differential display Neuroimmunomodulation 2, 347-355 (1995)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Kattus
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                                                                                             17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       similar to complement C1 inhibitor, mRNA
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                                                                                                                       /Clone_lib="IFNgamma-induced astrocyte ESTs"
/note="cDNA from IFNgamma-induced cultured rat astrocytes
/was screened by PCR differential display. Regulated cDNAs
were amplifed, sequenced and confirmed by dot-blots and
                                                                                                 Northerns. * 25 c
                                                                                                                                                                                                  /clone="DR20"
                                                                                                                                                                                                            /strain="Sprague-Dawley"
/db_xref="taxon:10116"
                                                                                                                                                                                                                                            /organism="Rattus norvegicus"
                                                                                                                                                                                                                                                                              Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     normalization to a Cot = 5. Library constructed by Bento Soares and M.Fatima Bonaldo. RNA from 4 multiple sclerosis lesions from one patient was kindly provided by Dr. Kevin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    polylinker V_TYPE: phagemid; Site_1: Not I; Site_2: Eco
; 1st strand cDNA was primed with a Not I - oligo(dT)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        lesions from one patient was kindly provided G. Becker (NINDS/NIH). "
25 c 18 g 17 t
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               DB 158;
2.2;
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AI864984.1
                                             wk06cll.xl
similar to
                                                                              AI864984
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CDNA Library Preparation: David B. Krizman, Ph.D.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M. A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
Insert Length: 801 Std Error: 0.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Onpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
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Seq primer: -40ml3 fwd. ET from Amersham
High quality sequence stop: 84.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Tissue Procurement: Christopher A. Moskaluk, M.D., Emmert-Buck, M.D., Ph.D.
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National Cancer Institute, Cancer Genome Anat
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                                                                                                                                                                                                                                                                                                                       56:5380-5383.*
                                                                                                                                                                                                                                                                                                                                                /note="Vector: pAMP10; mRNA made from invasive ovarian tumor, cDNA made by oligo-d7 priming. Non-directional cloned. Size-selected on agarose gel, average insert cloned. Reference: Krizman et al. (1996) Cancer Reseation
                                                                                                                                                                                                                                                                                                                                                                                                                     /tissue_type="ovary"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /clone="IMAGE:1373352"
/clone_lib="NCI_CGAP_Ov2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism="Homo sapiens"
/db_xref="taxon:9606"
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                                                     90 bp mRNA EST 21-DEC-1999 NCI_CGAP_Lym12 Homo sapiens cDNA clone IMAGE:2411540 3'
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               GI:5529091
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Pred. No. 2.2;
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                                           repetitive element;, mRNA
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AA457423
IMAGE Consortium (info@image.llnl.gov) for Seq primer: -28m13 rev1 ET from Amersham High quality sequence stop: 76.
                                                                                                                                                                                                     Schellenberg, K., Steptoe, M.,
,T., Waterston, R. and Wilson, R.
Washu-Merck EST project 1997
Unpublished (1997)
                                                                                                                                                                                                                                                                                  l (bases 1 to 95)
Hillier,L., Allen,M., Bowle
Kucaba,T., Lacy,M., Le,N.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Life Technologies catalog #: 11547-015.
DNA Sequencing by: Washington University Genome
Clone distribution: NCI-CGAP clone distribution
found through the I.M.A.G.E. Consortium/LLNL at:
                               This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                Email: est@watson.wustl.edu
                                                                                                   Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                     Washington University Scho
                                                                                                                                                                                    Contact: Wilson RK
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
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Insert Length: 195 Std Error: 0.00
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National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae
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/clone="IMAGE:2411540"
/clone_lib="NCI_CGAP_Lym12"
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                                                                                                                                          School of Medicine way, Box 8501, St. 1
                                                                                                                                                                                                                                                          Bowles,L., Dubuque,T., Geisel,G., Jost,S.,
e,N., Lennon,G., Marra,M., Martin,J., Moore,B.
eptoe,M., Tan,F., Theising,B., White,Y., Wylie
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RESULT 8
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                                                                                                                                                                                                                                                                                                                                Email: est@watson.wustl.edu
This clone is available royalty-free through LLNL;
IMAGE Consortium (info@image.llnl.gov) for further j
Seq primer: -40ml3 fwd. ET from Amersham.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     White,Y., Wylie,T., WaterstowashU-NCI human EST Project Unpublished (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AA835205 101 bp mRNA EST 23-FEB-1999 ak64h01.sl Barstead pancreas HPLRB1 Homo sapiens cDNA clone IMAGE:1412689 3' similar to contains Alu repetitive element contains element KER repetitive element; mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hillier, L., Allen, M., Bowles, L., Dubuque, T., Geisel, G., Jost, S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Contact: Wilson RK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Krizman,D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens
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314 286 1810
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[AATTCGGATCCTTG], digested with Not
Not I and Eco RI sites of the modif
Library constructed by Bob Barstead.
                                                                                                                                           with a modified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="Organ: pancreas; Vector: pT7T3D-Pac (Pharmacia)
with a modified polylinker; Site_1: EcoRI; Site_2: Not
lst strand cDNA was primed with a Not I - oligo(dT) pr
                                                                                                                                                                                                                                                      /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:1412689"
                                                                           dev_stage="adult, 34 years"
lab_host="DH10B"
                                                                                                                                                                                                                       sex="female"
                                                                                                                                                                                                                                  clone_lib="Barstead pancreas HPLRB1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /clone="IMAGE:838155"
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B., Schellenberg,K., Steptoe,M., Tan,F., Theising,B.,
ylle,T., Waterston,R. and Wilson,R.
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                                     double-stranded cDNA was ligated to Eco RI adaptors CGGATCCTTG], digested with Not I and cloned into the
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                 the modified pT7T3 vector
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   cDNA Library Preparation: David B. Krizman, Ph.D. cDNA Library Arrayed by: Genome Systems Inc., Greg Lennon, Ph.D. DNA Sequencing by: Washington University Genome Sequencing Center Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

www-bio.llnl.gov/bbrp/image/image.html
Insert Length: 757 Std Error: 0.00
Seq primer: -40ml3 fwd. ET from Amersham
High quality sequence stop: 88.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AA604960 102 bp mRNA
no93b10.s1 NCI_CGAP_PI2 Homo sapiens cDNA clone IMAGE:1114363
similar to contains Alu repetitive element;contains element MER22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Tissue Procurement: W. Marston Linehan, M.D., Rodrigo Chuaqui, M.D., Michael Emmert-Buck, M.D., Ph.D.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Unpublished (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
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                   14
                            /dev_stage="45 years old"
//lab_host="DH1(DB"
//lab_host="DH1(DB"
//lab_host="DH1(DB"); Site_1: Not1; Site_2: EcoRI; 1st
strand cDNA was primed with oligo(dT)17 on 50 ng of
DNAse-treated, total cellular RNA obtained from 5,000-10
.000 microdissected preneoplastic cells
histologically-determined to be prostatic intraepithelial
neoplasia 2 (PIN2) cells. Double-stranded cDNA was
ligated to EcoRI adaptors, 5 cycles of PCR applied to the
cDNA with an adaptor-specific primer, and the resulting
PCR product subcloned into pAMP10 by the UDG-cloning
method (Life Technologies). Average insert size is 600
bp. NOTE: Not directionally cloned. This library was
constructed by David Krizman."
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               constructed by 1
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/db_xref="taxon:9606"
/clone="IMAGE:1114363"
/clone_11b="NCI_CGAP_Pr2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
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Query Match Best Local

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Similarity

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Pred. No. 2

DB 9; 2.2;

Length 102;

Mismatches

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18; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                cDNA Library Preparation: David B. Krizman, Ph.D. CDNA Library Arrayed by: Genome Systems Inc., Greg Lennon, Ph.D. DNA Sequencing by: Washington University Genome Sequencing Cente Clone distribution: NCI-CGAP clone distribution information can found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AA228795 103 bp mRNA EST 20-AUG-1997 nc14e07.sl NCI_CGAP_Pr1 Homo sapiens cDNA clone IMAGE:1008132 similar to contains alu repetitive element;contains element MER28
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Seg primer: -41ml3 fwd. ET from Amersh
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Unpublished (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Tumor Gene Index
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 National Cancer Institute,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
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1 (bases 1 to 103)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  strand cDNA was primed with oligo(dT)17 on 50 ng of DNAse-treated, total cellular RNA obtained from 5,000-10,000 microdissected, histologically normal prostate epithelial cells. Double-stranded cDNA was ligated to EcoRI adaptors, 5 cycles of PCR applied to the cDNA with an adaptor-specific primer, and the resulting PCR product subcloned into paMP10 by the UDG-cloning method (Life Fechnologies). Average insert size is 600 bp. NOTE: Not directionally closed with the contract co
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       directionally cloned. David Krizman."
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/db_xref="taxon:9606"
/clone="IMAGE:1008132"
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Human fetal heart,
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                        Homo
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7089e07.x1
similar to
                                                                        Tissue Procurement: Christopher Moskaluk, M.D., Emmert-Buck, M.D., Ph.D.
                                                                                                                       Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                         BF194862.1
EST.
cDNA Library Preparation: M. Bento Soares, Ph.D. cDNA Library Arrayed by: Greg Lennon, Ph.D. cDNA Sequencing by: Washington University Genome Sequencing Center Clone distribution: MCI-CGAP clone distribution information can be
                                                                                                          Email: cgapbs-r@mail.nih.gov
                                                                                                                                                                         NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anat
                                                                                                                                                                                                                                                   Eukaryota; Metazoa;
                                                                                                                                                                                                                                                                     Homo sapiens
                                                                                                                                                                                                                                                                                                                                            BF194862
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                                                                                                                                                                                                                                 Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BACKWARD: 5' CCAGTGAATTGTAATACGACTCACTATAGGGCG
Seq primer: 5' GAAATTAACCCTCACTAAAGGG 3'.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  rUKWARD: 5' GCCAAGCTCGAAATTAACCCTCACTAAAGGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Email: liewcc@utcc.utoronto.ca
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Fax: 4169785650
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Department of Laboratory Medicine and Pathobiology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Contact: Liew CC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Unpublished (1997)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Liew, C.C.
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1 (bases 1 to 105)
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adaptor-primer. Econ. ....

digestion with xhoI, for direct.

predigested lambda ZAP Express.

predigested 26 g 19 t
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/lab_host="E. coli XLI-Blue"
/note="Vector: Lambda ZAP Express; Site_1: EcoRI; Site_2:
/note-"Vector: Lambda ZAP Express; Site_1: EcoRI; Site_2:
XhoI; mRNA was purified from human fetal hearts (8-10
weeks). cDNA was synthesized using a XhoI-Oligo dT
adaptor-primer. EcoRI adaptors were ligated, followed by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Homo sapiens"
/db_xref="taxon:9606"
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                                                                                                                                                                                                                                                                                                                                                      repetitive element;,
                                                                                                                                                                                                                                                                                                                                                                                            mRNA
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                                                                                                                                                                                                                                                                                                                                                                        sapiens cDNA clone
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IMAGE:3643500 3'
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Consortium/LLNL, send

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AUTHORS
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Best Local
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Hiller,L., Lennon,G., Becker,M., Bonaldo,M.F., Chiapelli,B., Chissoe,S., Dietrich,N., DuBuque,T., Favello,A., Gish,W., Hawkins,M., Hultman,M., Kucaba,T., Lacy,M., Le,M., Le,N., Mardis,E., Moore,B., Morris,M., Parsons,J., Prange,C., Rifkin,L., Rohlfing,T., Schellenberg,K., Soares,M.B., Tan,F., Thierry-Meg,J., Trevaskis,E., Underwood,K., Wohldmann,P., Waterston,R., Wilson,R. and Marra,M. Genome Res. 6 (9), 807-828 (1996)
                                                                                                                                                                Seq primer: m13 -40 forward High quality sequence stop: 313.
                                                                                                                                                                                                      Source: IMAGE Consortium, LLNL This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                           Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      N23686 107 bp mRNA EST 28-DEC-1995
yw46a02.sl Weizmann Olfactory Epithelium Homo sapiens cDNA clone
IMAGE:255242 3' similar to contains Alu repetitive element;contains
element MER5 repetitive element; mRNA sequence.
                                                                                                                                                                                                                                                                                Email: est@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                    Contact: Wilson RK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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314 286 1810
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/organism-"Homo sapiens"
/db_xref-"GDB:3865651"
/db_xref-"taxon:9666"
/clone-"IMAGE:255242"
/clone_11b-"Weizmann Olfactory Epithelium"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1500552-1502855). Subtraction by Bento Soares and M. Fatima Bonaldo. * 19 c 31 g 26 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      a modified polylinker; Site_1: Not I; Site_2: Eco RI; Plasmid DNA from the normalized library NCI_CGAP_Kid3 was prepared, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from a pool of 5,000 clones made from the same library (cloneIDs 1322376-1333911, 1456007-1456775, and
                                                                                                                                              ocation/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /clone_"IMAGE:3643500"
/clone_lib="NCI_CGAP_Kidll"
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Best Local S
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                                                                                                                                                                                                                                                                                                                                                              Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. 1 Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               yw46b01.s1 Weizmann Olfactory Epithelium Homo sapiens cDNA clone IMAGE:255241 3' similar to contains Alu repetitive element;contains element MER5 repetitive element; mRNA sequence.
                                                                                                                                                                                                                                                                                                                                 High quality sequence stop: 342
                                                                                                                                                                                                                                                                                                                                                      IMAGE Consortium (info@image.llnl.gov)
Seq primer: m13 -40 forward
                                                                                                                                                                                                                                                                                                                                                                                                                                  Email: est@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Contact: Wilson RK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Genome Res. 6 (9), 807-828 (1996)
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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/sex="Pemale"
/fissue_Type="olfactory epithelium"
/fissue_Type="olfactory epithelium"
/dev_stage="35 year old"
/lab_host="SOLR cells (kanamycin resistant)"
/note="Organ: nose; Vector: pBluescript SK:; Site_1: EcoRI
/note="Organ: nose; Vector: pBluescript SK: Oligo
dT: Olfactory epithelium, normal. Average insert size: 0.8
kb; Uni-ZAP XR Vector: Library constructed by N. Walker,
kb; Uni-ZAP XR Vector: Tibrary constructed by N. Walker,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /clone_lib="Weizmann Olfactory Epithelium"
                                                                                                                                                                                                                  /clone="IMAGE:255241"
                                                                                                                                                                                                                                  /db_xref="taxon:9606"
                                                                                                                                                                                                                                                     /organism="Homo sapiens"
/db_xref="GDB:3865650"
                                                                                                                                                                                                                                                                                                              Location/Qualifiers
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/dev_stage="35 year old"
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Pred. No. 2
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Search completed: November 15, 2001, 06:39:19 Job time: 9295 sec
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AUTHORS
TITLE
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D82540
LOCUS
DEFINITION
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ORIGIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Institute for Molecular and Cellular Regulation, Gunma University 3-39-15 Showa-machi, Maebashi Gunma 371, Japan Tel: 272-20-8856 Fax: 272-20-8896
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human pancreatic islet ESTs
Unpublished (1995)
Contact: Jun Takeda
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 110)
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                                                                                                                                                                                                                                                                                                                                                                                                                                     jtakeda@sb.gunma-u.ac.jp.
Location/Qualifiers
                                                                                                                                                                                                                                              /clone_lib="Human pancreatic islet"
/clone_lib="Human pancreatic islet"
/clone_"Yector: Lambda ZAPII; Site_1: Eco RI; Site_2: Xho
I; mRNA was prepared from normal adult human islets. cDNA
was directionally synthesized from the Xho I in the vector
to the EcoRI site. cDNA was size fractionated to remove
sequences <1000 bp in size."
sequences <1000 bp in size."
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CTCGAGTTTTTTTTTTTTTTTTT 3'"
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/db_xref="taxon:9606"
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httve 0; Mismatches 0;
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Maximum DB seq length: 2000000000
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Perfect score:
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18
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gb_pr3:* gb_pr3:* gb_pr6:* gb_pr6:* gb_pr7:* gb_pr6:* gb_pr1:* gb_pr1:* gb_pr1:* gb_pr1:* gb_pr1:* gb_pr1:* gb_pr1:* gb_pr1:* gb_pr1:*	gb_htg11:* gb_htg12:* gb_htg13:* gb_htg14:* gb_htg15:* gb_htg15:* gb_htg17:* gb_htg17:* gb_htg19:* gb_htg20:* gb_htg21:* gb_htg21:* gb_htg22:* gb_htg23:* gb_htg23:* gb_htg23:* gb_htg23:* gb_htg24:*	95-97 95-97 95-11:* 95-12:* 95-14:* 95-14:* 95-14:* 95-14:* 95-14:* 95-14:* 95-14:* 95-14:* 95-14:* 95-14:* 96-14:*	em_pu:* em_ph:* em_pl:* em_pl:* em_ro:* em_ro:* em_sy:* em_sy:* em_un:* em_vi:* em_vi:* em_vi:* em_vi:* em_vi:* em_vi:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

c 8 7 6 5 4 3 2 1	Result No.
18 18 18 18 18 18 18	Score
100.0 100.0 100.0 100.0 100.0 100.0	Query Match Length DB
1107 1114 2224 2324 235 236 240	Length Di
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Best Local Similarity 100.
Matches 18; Conservative
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1 (bases 1 to 107)
Sinnett,D., Richer,C., Deragon,J.-M. and Labuda,D.
Alu RNA transcripts in human embryonal carcinoma cells. Model of post-transcriptional selection of master sequences
J. Mol. Biol. (1992) In press
                                                                                                                                                                                                                                                                                                                                                                                                                           HUMALCE162 107 bp ss-rNA PRI 15-APR-1994 Human carcinoma cell-derived Alu RNA transcript, clone CE162.
                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens male embryo carcinoma cDNA to other RNA.
                                                                                                                                                                                                                                                                                                                                                                                                  M87924.1 GI:174871
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/db_xref="taxon:9606"
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                                                                                                 tissue_type="carcinoma"
30 c 35 g 1
                                                                                                                                 /sex="male"
      100.0%; Sc
100.0%; P;
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261176 H.sapiens C
X55932 Human DNA f
U18390 Human Alu s
U67831 Human prima
U67827 Human prima
AL162993 H.sapiens
I51997 Sequence 5
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U14705 Human Alu-S
U14709 Pan troglod
Z62833 H.sapiens C
U1838 Human Alu s
X55933 Human DNA f
X75333 H.sapiens A
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U14568 ***ALU WARN
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Sinnett,D., Richer,C., Deragon,J.-M. and Labuda,D.
                                                                                                                                                                                                  post-transcriptional selection of master sequences
J. Mol. Biol. (1992) In press
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                Homo sapiens male embryo carcinoma cDNA to other RNA Homo sapiens
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Sinnett, D., Richer, C., Deragon, J.-M. and Labuda, D.
Alu RNA transcripts in human embryonal carcinoma cells. Model
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J. Mol. Biol. (1992) In press
    Location/Qualifiers
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Human carcinoma cell-derived Alu RNA transcript, clone CE44.
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                                                                             tissue_type="carcinoma" 39 c 44 g 2
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/db_xref="taxon:9606"
/cell_line="NTera2D1"
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/db_xref="taxon:9606"
/cell_line="NTera2D1"
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/sex="male"
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REFERENCE AUTHORS TITLE

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                                                                                                                                                              Human clone 4 Alu rep
U02063
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                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutele
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
1 (bases 1 to 234)
                                                                                                                                                       002063.1
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Submitted (16-OCT-1995) The Sanger Centre, Hinxton, Cambridgeshire,
CB10 1RQ, England. E-mail contact: humquery@sanger.ac.uk
                                    methylation
                                        Alu transcripts: cytoplasmic localisation and regulation by DNA
                                                         Liu, W.M., Maraia, R.J., Rubin, C.M. and Schmid, C.W.
                                                                                                               Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2 (bases 1 to 224)
Cross,S.H., Charlton,J.A., Nan,X.
Purification of CpG islands using
Nat. Genet. 6 (3), 236-244 (1994)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 (bases 1 to 224)
Dodsworth, S.J., Huckle, E., Wilkinson, P. and Micklem, G
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CpG island; genomic Msel fragment.
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H.sapiens CpG island DNA genomic Msel fragment,
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/tissue_type="blood"
/clone_lib="CGI-1"
/clone="178h6"
a 61 c 55 g
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/db_xref="taxon:9606"
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Direct Submission
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Liu,W.M.
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Similarity 100.0%;
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(bases 1 to 235)
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                            22. .215
/standard_name="NRL-402R"
/note="STS PCR product"
                                      /PCR_conditions="95deg.
1.0min"
                                                                                                        /map="3p21.3"
                                                                                                                                               /chromosome="3"
                                                                                                                                                                                                Location/Qualifiers
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Animal Genetics, N.I.Vavilov Institute of General Genetics RAS, Gubkin Str. 3, Moscow B-333, 117809 GSP-1, RUSSIA The STS markers recistered took
                                                                                                                                                                                                                                                                                           Institute of the Russian Academy of Sciences. The Not! clones were used to construct Not! map of human chromosome 3 by FISH and mapping by a somatic cell hybrid panel.
                                                                                                                                                                                                                                                                                                                                                                                      3 received by E.R. Zabarovsky (Karolinska
Institute, Sweden) as a result of collaborative
research work with Engelhardt Molecular Biology
                                                                                                                                                                                                                                                                                                                                                                                                                                                           The STS markers registered were developed to clones from Notl library of human chromosome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sulimova,G.E., Udina,I.G., Kunizheva,S.S. and Kompaniitzev,A.A. Creating NotI-STS Markers for Human Chromosome 3 Mol. Biol. 33, 698-703 (1999)
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Submitted (23-SEP-1993) University of and Cellular Biology, Davis, CA 95616
Location/Qualifiers
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Mammalia; Eutheria; Primates;
/note="NRL-402R forward primer"
/PCR_conditions="95deg. 0.8min,
                                                                                                                            /cell_type="mouse/human microcell
/cell_line="MCH903.1"
                                                                                                                                                                                                /organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                         clone_lib="NotI-linking library'
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/cell_type="epithelial cell"
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/db_xref="taxon:9606"
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  0.8min, 72deg.
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            Homo sapiens
Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                         HSU02050 240 bp
Human clone AZA7 Alu
                                                                                                                                                                                                         l Similarity
18; Conserva
                                                                                                     HSU02050
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; 1 (bases 1 to 236)
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    (bases 1 to 240)
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                                                                      GI:406885
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Location/Qualifiers
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/note="NRL-402R reverse primer"
/PCR_conditions="95deg. 0.8min,
1.0min"
                                                                                                                                                                                                                                                                                              cell_type="epithelial cell"
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/db_xref="taxon:9606"
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Primates;
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No.
            Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                          38 t
                                                                                                                                                                                                                                                                                                                                                                                      ., University of California, Davis, Davis, CA 95616 USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0.73;
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BASE COUNT 60
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AF034649
                                                                                                                                                                                                                                                                   Submitted (13-NOV-1997) Pediatry, University of Montreal, Sainte-Justine Hospital, Research Center (Charles Bruneau Center of Cancerology), 3175 Cote Sainte-Catherine, Montreal, Quebec H3T-1C5,
                                                                                                                                        reverse primer: 5'-ttttttgagacggagtctcgctc-3'...
Location/Qualifiers
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Zietkiewicz, E., Richer, C.
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Zietkiewicz,E., Richer,C
Phylogenetic affinities
                                                                                                                                                                                                                 Alu element are not included.
                                                                                                                                                                                                                                            Sequences corresponding to the
                                                                                                                                                                                                                                                                                                                       Direct Submission
                                                                                                                                                                                                                                                                                                                                                              Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Tarsius syrichta
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                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Eutheria; Primates; Tarsii; Tarsiidae; Tarsius.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   tarsier.
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                                                                                                                                                                                      primer:
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            /rpt_family="tarsier
/rpt_type=dispersed
69 c 78 g
                                                                                 /organism="Tarsius syrichta"
/db_xref="taxon:9478"
/clone="TARS25"
                                                                  note="PCR-amplified"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="AZA7"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /cell_type="epithelial cell"
1. .240
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /sex="female"
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Pred. No.
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TARS25 tarsier Alu.
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Best Local (
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                                                                                                                                                                                         188
                                                                                                                                                                                                                                           Local Similarity hes 18; Conserv
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 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 248)
                                                                                               Homo sapiens clone 18ptelc6.59t3 sequence. AF270578
                                           Homo sapiens
                                                                                    AF270578.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (18-OCT-1996) J. Gu, University Of North Carolina-Chapel Hill, Pharmacology, 1106 Flob Cb7365, North Carolina 27599, USA Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gu,J.J., Spychala,J. and Mitchell,B.S.
Regulation of the human inosine monophosphate dehydrogenase type gene. Utilization of alternative promoters
J. Biol. Chem. 272 (7), 4458-4466 (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Eutherla; Primates; Catarrhin1; Hominidae; Homo.

1 (bases 1 to 245)
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                                                                                                                                                                                                                                                                                                                                                                                                /cell_type="leukocyte"
/map="q31.3-q32"
/clone="phage 1111a"
/dev_stage="adult"
                                                                                                                                                                                                                                                                                                                                         /gene="inosine monophosphate dehydrogenase type I"
                                                                                                                                                                                                                                                                                                                                                                     gene="inosine monophosphate dehydrogenase type
                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="7"
                                                                                   GI:9755120
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O; Mismatches
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0.72;
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RESULT 13
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                                                                                                                                173 GGCGGAGCTTGCAGTGAG 190
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257 bp

H.Sapiens CpG island D

read cpg31b4.ftla.

260686
260686.1 GI:10327an
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Sinnett,D., Richer,C., Deragon,J.-M. and Labuda,D.
Alu RNA transcripts in human embryonal carcinoma cells. Model
post-transcriptional selection of master sequences
J. Mol. Biol. (1992) In press
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human carcinoma cell
M87925
M87925.1 GI:174872
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Alu repeat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Riethman,H.C. and Moyzis,R.K.
Direct Submission
Submitted (19-MAY-2000) Molecular Genetics, The Wistar Institute,
3601 Spruce St., Philadelphia, PA 19104, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens male embryo carcinoma cDNA to other RNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HUMALCE21
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity
                                                                                                                                                                                     Conservative
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                                                                                                                                                                                                                                                                                                                          /organism="Homo sapiens"
/db_xref="taxon:9606"
/cell_line="NTera2D1"
                                                                                                                                                                                                                                                                 /tissue_type="carcinoma"
66 c 80 g 37 t
                                                                                                                                                                                                                                                                                                /dev_stage="embryo"
/sex="male"
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74 c 55 g
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/map="18ptel"
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/db_xref="taxon:9606"
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                                                                                                                                                                                               Score 18; DB 97; Pred. No. 0.72;
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                                                          DNA
                                             genomic
                                                                                                                                                                                   Mismatches
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                                          Msel fragment,
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                                            clone 31b4, forward
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clone CE21.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            GGCGGAGCTTGCAGTGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  18;
                                                           Primer B: TC
STS size: 81
                                                                                      Email: pieter@dejong.med.buffalo.edu
Primer A: TTATTCTTAAGGGAAGAGGTTC
                                                                                                               Human Genetics Department
Roswell Park Cancer Institute
Elm and Carlton Streets, Buffalo,
Tel: 716-845-3168
Fax: 716-845-8449
                                                                                                                                                                                                                                                                                                                                                                           G38317 262 bp
RPCI-4-790D12T7 Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (16-OCT-1995) The Sanger Centre, Hinxton, Cambridgeshire, CB10 IRQ, England. E-mail contact: humquery@sanger.ac.uk
2 (bases 1 to 257)
Cross,S.H., Charlton,J.A., Nan,X. and Bird,A.P.
Purification of CpG islands using a methylated DNA binding column Nat. Genet. 6 (3), 236-244 (1994)
                                                PCR Profile:
                                                                                                                                                                                Contact: Pieter J. de Jong
                                                                                                                                                                                                             Unpublished (1998)
                                                                                                                                                                                                                                         de Jong, P.J.
                                                                                                                                                                                                                                                Mammalia; Eutheria;
1 (bases 1 to 262)
                                                                                                                                                                                                                                                                                                                                      G38317.1
                                                                                                                                                                                                                                                                                                                                                                  site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Vector: pGEM-52f(-)
Clones are available from the UK MRC Human Genome Mapping Project
Resource Centre, Hinxton, Cambridgeshire CB10 1RQ, UK. See URL:
                                                                                                                                                                                                                                                                             Eukaryota; Metazoa;
                                                                                                                                                                                                                                                                                             Homo sapiens
                                                                                                                                                                                                                                                                                                           human.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      http://www.hgmp.mrc.ac.uk/ for details
or contact: biohelp@hgmp.mrc.ac.uk.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          94282070
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MacDonald,M., Huckle,E., Wilkinson,P. and Micklem,G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Direct Submission
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human.
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                                                                                                                                                                                                                        chromosome 14q24.3
     Annealing
                   Denaturation
                                Presoak:
                                                                          TCAGCCTCCTGATTTCAAAT
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87 c
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/clone_lib="CGI-1"
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Primates;
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Submitted (15-SEP-1994) Wojciech Makalowski, National Center for Submitted (1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human Alu-Sb2 repeat, U14706
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                           /rpt_family="Alu-Sb2"
/rpt_unit=1..262
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/evidence=experimental
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/db_xref="taxon:9606"
/clone="HUM-10"
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Search completed: November 15, 2001, 06:17:28 Job time: 8013 sec	Db 211 GCCGGAGCTTGCAGTGAG 228	Qy 1 ggcggagcttgcagtgag 18	Matches 18; Conservative 0; Mismatches 0; Indels	Query Match 100.0%; Score 18; DB 97; Length 262; Best Local Similarity 100.0%; pred. No. 0 72;
			Indels	Length 2
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Database :
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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RESULT 1 AC007684 LOCUS DEFINITION ACCESSION KEYNORDS SOURCE ORGANISM REFERENCE AUTHORS TITLE JOURNAL MEDLINE REFERENCE AUTHORS TITLE JOURNAL AUTHORS TITLE JOURNAL REFERENCE AUTHORS TITLE JOURNAL		0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0
ACO07684 196848 bp DNA PRI 21-DEC-1999 Romo sapiens BAC clone RP11-449G16 from 2, complete sequence. ACO07684 3 GI:5836173 ACO07684 4 GI:583617 ACO07684 4 GI:583617 ACO07684 4 GI:583617 ACO07684 5 GI:583617 ACO0	ALIGNMENTS	17 70.8 239254 76 AC079569 AC079569 Mus muscu 16 66.7 10.8 252746 76 AC079519 AC079519 Mus muscu 16 66.7 1223 8 TRCWPWH 16 66.7 3923 8 AB017819 AB017819 Theragra ch 16 66.7 3923 8 AB017819 AB017819 Theragra ch 16 66.7 3923 8 AB017819 AB017819 Theragra ch 16 66.7 11199 1 AB001138 AB017819 Theragra 16 66.7 23991 65 AC017994 AC015065 Mus muscu 16 66.7 38201 85 AC000046 AC001994 Drosophi1 16 66.7 38201 85 AC000046 AC001994 Drosophi1 16 66.7 38201 85 AC000048 AC015065 Drosophi1 16 66.7 11010 63 AC015386 AC0017994 AC015085 Drosophi1 16 66.7 11010 63 AC015386 AC0017944 AC005744 Homo sapi 16 66.7 11010 68 AC0015386 AC0017994 AC015386 Drosophi1 16 66.7 11010 68 AC0015386 AC0017994 AC015386 Drosophi1 16 66.7 11010 68 AC0015381 AC001750 Drosophi1 17 66.7 11010 68 AC0015381 AC002013 Homo sapi 18 66.7 11010 68 AC004351 AC002033 AC007150 Drosophi1 19 66.7 154548 80 AL133419 AC002033 AC002033 Homo sapi 19 66.7 154549 80 AC035927 AL365257 Homo sapi 19 66.7 156150 69 AC025602 10 66.7 15944 AC005247 AC005247 AC005247 AC0052577 AL365257 Homo sapi 19 66.7 163162 4 AC005247 AC005247 Drosophi1 19 66.7 163162 4 AC005247 AC005281 Homo sapi 19 66.7 163163 73 AC067805 AC013584 Homo sapi 19 66.7 163163 73 AC068430 AC015992 Homo sapi 10 66.7 168131 69 AC025982 11 66.7 168131 69 AC025982 11 66.7 168131 69 AC025982 12 AC005282 Homo sapi 13 AC067365 AC013584 AC005361 Homo sapi 14 AC073659 AC025982 Homo sapi 15 AC073659 AC025982 Homo sapi 16 AC7 168131 69 AC025982 17 AC00544 AC00544 AC005454 AC005869 Homo sapi 17 AC055821 Homo sapi 18 AC7 16811 69 AC025982 18 AC073654 AC005864 AC005865 Homo sapi 18 AC7 168134 80 AC021654 AC005865 AC0216
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                                                                                                                                                                                         Direct Submission

Submitted (21-DEC-1999) Department of Genetics, Washington
University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA
On Sep 8, 1999 this sequence version replaced gi:5001493.
                                                                                                                                                                                                                                                                                                                                                        Waterston, R.
                                                                                                                                                                                                                                                                                                                                                                             MO 63108, USA
5 (bases 1 to 196848)
  NOTICE:
                                                                                               Web site: http://genome.wustl.edu/gsc
Contact: sapiens@watson.wustl.edu
------ Summary Statistics
                                                                                                                                                                              Center: Washington University Genome Sequencing Center Center code: WUGSC
                                                                             Center project name: H_NH0449G16
This sequence may not represent the entire insert of this
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This sequence was finished as follows unless otherwise noted: all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one subclone; and the assembly was confirmed by clone. It may be shorter because we only sequence overlapping clone sections once, or longer because we provide a small overlap between neighboring data submissions.

restriction digest.

MAPPING INFORMATION:
Mapping information for this clone was provided by Dr. John D.
Mapping, information for this clone was provided by Dr. John D.
MCPherson, Department of Genetics, Washington University, St. Louis
MO. For additional information about the map position of this
sequence, see http://genome.wustl.edu/gsc

SOURCE INFORMATION:

The RPCI-11 human BAC library was made from the blood of one male donor, as described by Osoegawa, K., Woon, P.Y., Zhao, B., Frengen, E., Tateno, M., Catanese, J.J. and de Jong, P.J. (1998) An improved approach for construction of bacterial artificial chromosome libraries. Genomics 51:1-8. The clone may be obtained either from Research Genetics, Inc. (http://www.resgen.com) or Pieter de Jong and coworkers at the Roswell Park Cancer Institute (http://bacpac.med.buffalo.edu)
VECTOR: pBACe3.6

NEIGHBORING SEQUENCE INFORMATION:
The clone sequenced to the left is RP11-395B14. Actual start of this clone is at base position 1 of RP11-449G16; actual end is at base position 196848 of RP11-449G16.

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AUTHORS
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Direct Submission
Submitted (15-DEC-2000) DNA Sequencing and Technology Center,
Stanford University, 855 California Avenue, Palo Alto, CA 94304,
                                                       3 (bases 1 to 49306)
Abola,A.P., Bruno,D., Conn,L., Dela Rosa,M., Faulkner,D.,
Federspiel,N., Glukhov,S., Hansen,N., Herman,Z.S., Hyman,R.,
Lam,B., Mao,J., Marathe,R., Miranda,M., Morehouse,A.J., Nguyen,M.,
Oefner,P., Palm,C.J., Ramirez,D., Southwick,A.M., Wilhelmy,J.,
Yu,S. and Davis,R.W.
                                                                                                                                                               Submitted (27-JAN-2000) DNA Sequencing and Technology Center, Stanford University, 855 California Avenue, Palo Alto, CA 94304,
                                                                                                                                                                                                                                                                                                           Mao,J., Lam,B., Marathe,R., Miranda,M., Morehouse,A.J., Hyman,R.,
Oefner,P., Palm,C.J., Ramirez,D., Southwick,A.M., Wilhelmy,J.,
YUS,S. and Davis,R.W.
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                                                                                                                                                                                                                                                                          Unpublished (bases 1 to 49306)
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Birren, B., Linton, L., Nusbaum, C., Lander, E., Allen, N., Anderson, S., Barran, B., Bastlen, V., Boguslawily, L., Boukhgalter, B., Brown, A., Camarotata, J., Campopiano, A., Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S., Dodge, S., Faro, S., Ferreira, P., FitzHugh, W., Gage, D., Galagan, J., Gardyn, S., Ginde, S., Goyette, M., Graham, L., Grand-Pierre, N., Gardyn, S., Ginde, S., Hotton, L., Hulme, W., Illev, I., Johnson, R., Jones, C., Karatas, A., LaRocque, K., Lamazares, R., Landers, T., Lehoczky, J., Levine, R., Liu, G., MacLean, C., McKarnan, K., Marpheeters, R., Meldrim, J., Meneus, L., Mihova, T., Mienga, V., Murphy, T., Naylor, J., Nguyen, C., Norbu, C., Norman, C.H., Phunkhang, P., Pierre, N., Pollara, V., Raymond, C., Retta, R.,
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Birren, B., Linton, L., Nusbaum, C. and Lander, E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      all regions were double stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE SAMPLING. AC087465
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Center clone name: RP11-323C17
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/db_xref="taxon:9606"
/chromosome="5"
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Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (05-JAN-2001) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA On Apr 12, 2001 this sequence version replaced gi:12039478.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Rieback, M., Riley, R., Rise, C., Rogov, P., Roman, J., Rosett Roy, A., Santos, R., Schauer, S., Schupback, R., Seaman, S., Sougnez, C., Spencer, B., Stange-Thomann, N., Stojanovic, N.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Direct Submission
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NOTE: This record contains 76 individual sequencing reads that have not been assembled into contigs. Runs of N are used to separate the reads and the order in which they appear is completely arbitrary. Low-pass sequence sampling is useful for identifying clones that may be gene-rich and allows
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Center clone name: 94_P_14
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                                                                                                                                                                                                                                                                                                                                                                         6478: contig of 710 bp in length
6479 6578: gap of 100 bp
6579 7284: contig of 706 bp in length
7285 7384: gap of 100 bp
7385 8133: contig of 749 bp in length
8134 8233: gap of 100 bp
9234 8982: contig of 749 bp in length
983 9082: gap of 100 bp
983 9082: contig of 749 bp in length
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     14063 14802: contig of 740 bp in length
14803 14902: gap of 100 bp
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14903 15649: contig of 747 bp in length
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183 3382: contig of 751 b
183 3382: gap of 100 bp
83 4099: contig of 717 by
90 4199: gap of
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9832: contig of 750 bp in
32: gap of 100 bp
10659: contig of 727 bp in
16456: contig of
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099: contig of 717 bp
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42908: contig of 580 bp
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9811: gap of 100 bp 1
40543: contig of 732 bp 1
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36415: contig of 755 bp
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34724: contig of 748 bp
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3556: contig of 736 bp
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33063: contig of 746 bp in length
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33876: contig of 713 bp in length
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28884: contig of 733 bp in length
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23898: contig of 737 bp
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6: contig of 725 bp in length
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contig of 750 bp in length
jap of 100 bp
7: contig of 721 bp in length
gap of 100 bp
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contig of 717 bp in length
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96: contig of
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51: contig of 701
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15: contig of 706
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Best Local
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                        Sequencing vector: M13; 78% Sequencing vector: plasmid; 22% Sequencing vector: plasmid; 22% Chemistry: Dye-trimer ET; 78% of reads Chemistry: Dye-terminator Big Dye; 22% of reads Assembly program: Phrap; version 0.990319
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On Mar 13,
                                                                                                                                                                                                                         Submitted (04-DEC-1999) Genome Sequencing Center, Washington University School of Medicine, 4444 Forest Park Parkway, St. MO 63108, USA
                                                                                                             Center project name: H_NH0094P14
                                                                                                                                                    Center: Washington University Center code: WUGSC
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Waterston, R.H.
                                                                                                                                                                                                                                                                  Direct Submission
                                                                                                                                                                                                                                                                                                         Unpublished
                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                       HTG;
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HOMO sapiens chromosome 15 clone RP11-94P14, WORKING DRAFT
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52109 52208: gap of 100 bp

52209 52949: contig of 741 bp in le

52950 53049: gap of 100 bp

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54732 55669: contig of 738. bp in le
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50475: contig of 748 bp
50575: gap of 100 bp
51296: contig of 721 bp
                                                                                                                                                                                                     2000 this sequence version replaced gi:6838893
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57177: contig of 757
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55569: gap of 100 bp
56320: contig of 751 bp
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03: gap of 100 1
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150210 bases at least Q40
153841 bases at least Q30
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f 751 bp in length
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be preserved.
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                                                                        /note="assembly_name:Contig16"
25799. .32439
                                                                                                      18853.
                                                                                                                                                                                                                                                                                                        /organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="15"
                         note="assembly_name:Contig18"
                                                       note="assembly_name:Contig17"
                                                                                                             note="assembly_name:Contig15"
                                                                                                                                                                                                                             note="assembly_name:Contigl1"
                                                                                                                                           note="assembly_name:Contig14"
                                                                                                                                                                                                                                                                                          clone="RP11-94P14"
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"assembly_name:Contig19"
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1906: gap of unknown length
3900: contig of 1994 bp in length
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                                                                                                                                                                                                     Direct Submission
Submitted (01-MAR-2001) DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
On Mar 1, 2001 this sequence version replaced gi:8576139.
Draft Sequence Produced by DOE Joint Genome Institute
WWW.jgi.doe.gov
                                                                                                                              www-shgc.stanford.edu
Quality: Phrap Quality >=40 99.8% of Sequence;
Estimated Total Number of Errors is 0.2.
                                                                                                                                                                                 Finishing Completed at Stanford Human Genome Center
                                                                                                                                                                                                                                                                                                   Submitted (29-FEB-2000) Production Sequencing Facility, DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA 3 (bases 1 to 170264)
DOE Joint Genome Institute and Stanford Human Genome Center.
                                                                                                                                                                                                                                                                                                                                                                                            2 (bases 1 to 170264)
DOE Joint Genome Institute.
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DOE Joint Genome Institute and Stanford Human Genome Center.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                            /chromosome="5"
/clone="RP11-42L13"
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/db_xref="taxon:9606"
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104184. .120979
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87195. .104083
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143161. .161492
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                29650 с
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Query Match Best Local Similarity

75.0%; 100.0%;

Score 18; Pred. No.

DB 88; 6.1;

Length 170264;

VERSION KEYWORDS

ACCESSION DEFINITION

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (20-APR-2000) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA On Jan 10, 2001 this sequence version replaced gi:7798794. All repeats were identified using RepeatMasker:.

Smit, A.F.A. & Green, P. (1996-1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Roy,A., Santos,R., Schauer,S., Severy,P., Spencer,B., Roy,A., Santos,R., Schauer,S., Subramanian,A., Talamas,J., Stange-Thomann,N., Stojanovic,N., Subramanian,A., Talamas,J., Tesfaye,S., Theodore,J., Tirrell,A., Travers,M., Trigillo,J., Tesfaye,S., Theodore,J., Tirrell,A., Travers,M., Trigillo,J., Vassillev,H., Viel,R., Vo,A., Wilson,B., Wu,X., Wyman,D., Ye
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Levine, R., Lieu, C., Liu, G., Locke, K., Macdonald, P., Marquis, N., McCarthy, M., McEwan, P., McGurk, A., McKernan, K., McPheeters, R., McCarthy, M., McEwan, P., McGurk, A., McKernan, K., McPheeters, R., Meldrim, J., Meneus, L., Mihovar, Miranda, C., Mienga, V., Morrow, J., Murphy, T., Naylor, J., Norman, C. H., O'Connor, T., O'Connell, P., O'Nell, D., Olivar, T. M., Oliver, J., Peterson, K., Pierre, N., Pisanl, C., Pollara, V., Raymond, C., Riley, R., Rogov, P., Rothman, D., Pisanl, C., Pollara, V., Raymond, C., Riley, R., Rogov, P., Rothman, D., Pisanl, C., Pollara, V., Raymond, C., Riley, R., Rogov, P., Rothman, D., Pisanl, C., Pollara, V., Raymond, C., Riley, R., Rogov, P., Rothman, D., Pisanl, C., Pollara, V., Raymond, C., Riley, R., Rogov, P., Rothman, D., Pisanl, C., Pollara, V., Raymond, C., Riley, R., Rogov, P., Rothman, D., Pisanl, C., Pollara, V., Raymond, C., Riley, R., Rogov, P., Rothman, D., Pisanl, C., Pollara, V., Raymond, C., Riley, R., Rogov, P., Rothman, D., Pisanl, C., Pollara, V., Raymond, C., Riley, R., Rogov, P., Rothman, D., Pisanl, C., Pollara, V., Raymond, C., Riley, R., Rogov, P., Rothman, D., Pisanl, C., Pollara, V., Raymond, C., Riley, R., Rogov, P., Rothman, D., Pisanl, C., Pollara, V., Raymond, C., Riley, R., Rogov, P., Rothman, D., Pisanl, C., Pollara, V., Raymond, C., Riley, R., Rogov, P., Rothman, D., Pisanl, C., Pollara, V., Raymond, C., Riley, R., Rogov, P., Rothman, D., Pisanl, C., Pollara, V., Raymond, C., Riley, R., Rogov, P., Rothman, D., Pisanl, C., Pollara, V., Raymond, C., Riley, R., Rogov, P., Rothman, P., Rogov, P., R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Galagan, J., Gardyna, S., Ginde, S., Goyette, M., Graham, L., Grand-Pierre, N., Grant, G., Hagos, B., Heaford, A., Horton, L., Howland, J.C., Illev, I., Johnson, R., Jones, C., Kann, L., Karatas, A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Anderson, S., Baldwin, J., Barna, N., Bastien, V., Beda, F., Boguslavkly, L., Boukhgalter, B., Brown, A., Burkett, G., Campopiano, A., Castle, A., Choepel, Y., Colangelo, M., Collins Collymore, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Dodge,S., Domino,M., Doyle,M., Ferreira,P., FitzHugh,W., Gage,D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bomo sapiens chromosome 4 clone RP11-741G21 map 4, WORKING DRAFT
                                                                                                Sequencing vector: M13; M77815; 49% of reads Sequencing vector: Plasmid; n/a; 51% of reads Sequencing vector: Plasmid; n/a; 51% of reads Chemistry: Dye-terminator Big Dye; 100% of reads Assembly program: Phrap; version 0.960731 Consensus quality: 199511 bases at least Q40 Consensus quality: 201020 bases at least Q30 Consensus quality: 201685 bases at least Q20 Insert size: 194000; agarose-fp Insert size: 202215; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Birren, B., Linton, L., Nusbaum, C., Lander, E., Abraham, H., Allen, N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Birren, B., Linton, L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE, 8 unordered pieces
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AC060773
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AC060773.3 GI:12061518
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (bases 1 to 202915)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       repeats were identified using RepeatMasker.
L.A.F.A. & Green, P. (1996-1997)
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in, J., LaRocque, K., Lamazares, R., Landers, T., Lehoczky, J
                                     Quality coverage: 9.5 in Q20 bases; agarose-fp Quality coverage: 9.1 in Q20 b.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Center clone name: 741_G_21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Center project name: L7430
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Contact: sequence_submissions@genome.wi.mit.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ₩eb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Center code: WIBR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Center: Whitehead Institute/ MIT Center
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            //ftp.genome.washington.edu/RM/RepeatMasker.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    site:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ---- Project Information
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Zainoun, J., Zimmer, A. and Zody, M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 202915 bp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             http://www-seq.wi.mit.edu
          working draft' sequence. It currently
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4, clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         and Lander, E. RP11-741G21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           for Genome Research
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Talamas,J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Collins, S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ye, W.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0;
                                                                                                                                                                                                                                  RESULT
AF235106
LOCUS
                                                                                                   VERSION
                                                                                                                                      ACCESSION
                                                                                                                                                                                                    DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                 Db 188527 CAGATTTATTTTGGGCTT 188544
                                                                 KEYWORDS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
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Best Local Similarity
ORGANISM
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                                                                                                                                                                                                                                                                                                                                                                                                                                   2 cagatttattttgggctt 19
                                                                                                                                                       AF235106 141292 bp
Homo sapiens chromosome
WORKING DRAFT SEQUENCE,
Homo sapiens
                                                          AF235106.2 GI:8151913
HTG; HTGS_PHASE1; HTGS_DRAFT
                                                                                                                                      AF235106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61574 a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        consists of 8 contigs. The true order of the pieces is not known and their order in this sequence record
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
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109627 144431: contig of 34805 l
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            144432 144531:
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4060 5548; contig of 1489 bp in length
5549 5648; gap of 100 bp
5649 7747; contig of 2099 bp in length
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184286. .202915
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109627. 144/31
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/clone_lib="RPCI-11 Human Male BAC"
l. .3959
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="4"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              'note="assembly_fragment
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37018 c 37733 g
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202915: contig of 18630
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9: gap of 100 bp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         .75665
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9 8 map 8q12.3
9 unordered
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* NOTE: This is a 'working draft' sequence. It currently consists of 9 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
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3 (bases 1 to 141292)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (02-MAR-1999) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA On Mar 2, 1999 this sequence version replaced g1:4314281.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (25-FEB-1999) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                               /rpt_family="HERV23"
1961. .2607
complement(2544. .2680)
                                                                                                                                                                                        /rpt_family~"MER57B'
466. .519
                                                                                                                                                                                                                                                 complement (220.
                                  rpt_family="L1MC1"
                                                                                                                                                                                                                                                                                                                                                                                            /organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                                                                                                     rpt_tamily="LTR24B"
                                                                                                                                                                                                                                                                                                                                /clone_lib="RPCI-11 human BAC library"
                                                                                                                                                                                                                                                                                                                                                                   /clone-"hRPK.32_A_1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ocation/Qualifiers
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                                                                                                                                                                                                                                                                       family-"MER57-internal"
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complement(17141. .17494)
/rpt_family="LTR33"
                                                     /rpt_family="(TG)n"
20928. .21613
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complement(15553. .15801)
/rpt_family="Alusx"
                                                                                                                                                                                                                                                                                                                                                                                                  /rpt_family="Ricksha"
complement(14347..14615)
/rpt_family="Alusx"
                                        rpt_family="LTR8"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /rpt_family="AT_rich" complement(7627. .773
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="Single-stranded coverage."
complement(2608. .2873)
/rpt_family="MSTB"
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/rpt_family="L1"
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1, 791"
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5. .16574
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lement(11356. .11518)
_family="MIR"
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. .5995
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. .7037
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lement(4000
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lement(2899. .3023)
_family="MSTB"
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. . . 15513
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                                                                                                                                                 Ly-"AluSq"
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                            ACU/9569 239254 bp DNA HTG 02-SEP-2000 Mus musculus clone RP23-71M4, WORKING DRAFT SEQUENCE, 28 unordered pieces. ACU79569
                                                                                                                                                                                            l Similarity 100.
17; Conservative
AC079569.1 GI:9964934
HTG; HTGS_PHASE1; HTGS_DRAFT.
                                                                                                                                                                                                                                                                                                                                 /rpt_fanily="MER65B"

complement(43006. .43358)

/rpt_fanily="MER58B"

43880. .43913
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/rpt_family="(TTTG)n"
complement(22880. .23161)
/rpt_family="Aluy"
23307. .25586
                                                                                                                                                                                                                                                  /rpt_family="AluSx"
complement(46485. .46594)
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complement(46595. .46942)
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complement(42529, .426
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /rpt_family="(TTTTA)n" complement(36099...380
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complement(28398.
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/rpt_family="Aluy"
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                                                                                                                                                                                                                                                                                                                      _family="AT_rich"
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5. .38404
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4. .33477
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5. .26937
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Sequencing of Mouse
Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Consensus quality: 214511 bases at least Q40
Consensus quality: 225489 bases at least Q30
Consensus quality: 227597 bases at least Q30
Estimated insert size: 192000; agarose-fp estimation
Estimated insert size: 236554; sum-of-contigs estimation
Quality coverage: 9.6 in Q20 bases; agarose-fp estimation
Quality coverage: 7.79 in Q20 bases; sum-of-contigs estimation
* NOTE: This is a 'working draft' sequence. It currently
* consists of 28 contigs. The true order of the pieces
* is not known and their order in this sequence record is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Center: Joint Genome Institute
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (02-SEP-2000) Production Sequencing Facility, DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Summary Statistics
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Project Information
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Web site: http://www.jgi.doe.gov
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                 arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
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   Consensus quality:
Consensus quality:
Consensus quality:
                                                                                                                                               Center: Joint Genome Institute
Center Code: JGI
                                                                          Center Project Name: 1855075
Center clone name: RPCI-23_307N3
                                                                                                                                                                                  Direct Submission
Submitted (02-SEP-2000) Production Sequencing Facility, DOB Joint
Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
                                                 Summary Statistics
                                                                                                       Project Information
                                                                                                                                                                                                                                                                                           Mammalia; Eutheria; Rodentia;
1 (bases 1 to 252746)
DOB Joint Genome Institute.
                                                                                                                                   Web site: http://www.jgi.doe.gov
                                                                                                                                                                                                                                       2 (bases 1 to 252746)
DOE Joint Genome Institute.
                                                                                                                                                                                                                                                                                    Sequencing of Mouse
                                                                                                                                                                                                                                                                                                                                                          Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                           AC079519 252746 bp DNA HTG 02-SEP-2000 Mus musculus clone RP23-307N3, WORKING DRAFT SEQUENCE, 32 unordered
                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Eutherla; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                      HTG; HTGS_PHASE1; HTGS_DRAFT
                                                                                                                                                                                                                                                                                                                                                                                                      AC079519.1 GI:9964884
                                                                                                                                                                                                                                                                    Jnpublished
                                                                                                                                                                                                                                                                                                                                                                             nouse mouse.
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50089 c 50681 g 67592 t 2704 others
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/db_xref="taxon:10090"
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177486: contig of 18691 bp in
177586: gap of unknown length
203950: contig of 26364 bp in
204050: gap of unknown length
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* runs of N, but the exact sizes of the gaps are unknown.

* This record will be updated with the finished sequence is soon as it is available and the accession number.
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SOURCE
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TRCWPMH
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               BASE COUNT
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Best Local Similarity
Matches 17; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                           AUTHORS
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Kiyoyoshi Nishita, Hokkaido University, Department of Chemistry,
Faculty of Fisheries; 3-1-1, Minato-Cho, Hakodate, Hokkaido
041-861, Japan (E-mail:nishita@fish.hokudai.ac.jp,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei; Acanthomorpha; Paracanthopterygii; Gadiformes; Gadoidei; Gadidae; Teleostei; Metazone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Theragra chalcogramma skeletal muscle cDNA to mRNA Theragra chalcogramma
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                                                                                                                                                                                                                                                                                                                                                                                 Unpublished (1996)
                                                                                                                                                                                                                                                                                                                                                                                                                     Nishita, K.
                                                                                                                                                                                                                                                                                                                                                                                                                                         Tel:81-138-40-8800, Fax:81-138-40-8800)
2 (bases 1 to 1233)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Nishita, K.
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AtvnpykwlpvydQscvnayrgkkrmeapphifsvadnaygfmvtdrenqsclitges
Gagktvntkrvipvfativisgghkaadvgagkikgsledqiiaanplleaygnaktv
Rndnssrfgkfirihfhangkissadietylleksrvsfqlpdergyhiffqmmtnhk
                                               VTKGQTVPQVNNSVSALAKSIYERLFLWMVIRINTMLDTKQARQFYIGVLDIAGFEIF
                                                             PEIIEMTLITSNPYDFPMCSQGQITVASIDDKEELDATDAAIDILGFTSEDKVAIFKF
TGAVLHHGNMKFKQKQREEQAEPDGNEEADKICYLLSLNSADMLKALCYPRVKVQNEY
                                                                                                                                                                                 /product="myosin head"
/protein_id="BAA12887.1"
/db_xref="GI:1396064"
                                                                                                                                                                                                                                                                               /organism="Theragra chalcogramma"
/db_xref="taxon:48550"
/tissue_type="skeletal muscle"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Mus musculus"
/db_xref="taxon:10090"
/clone="RPZ3-30713"
/clone_lib="RPCI mouse BAC library 23"
/clone_lib="RPCI mouse BAC library 23"
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Conservative

66.7%; Pr 100.0%; Pr

Score 16; Pred. No.

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Length 1233;

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AB017819 3923 bp mRNA for myosin heavy chain, partial cds.

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16; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Determination of Primary Structure Walleye Pollack Myosin Heavy Chain Fish. Sci. (1998) In press
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ojima,T., Kawashima,N., Inoue,A., Amauchi,A., Togashi,M., Watabe, and Nishita,K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Nishita, K., Ojima, T. and Watabe, S. Direct Submission.
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Theragra chalcogramma skeletal muscle cDNA to mRNA.
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ATDAALDILGFTSEDKVAIFKTGAVLHGNMKFKOKOREEQAEPDGNEEADKICYLL
SLNSADMLKALCYPRVKVGNEYVTKGQTVPOVNNSVSALAKSIYERLFLMMYIRINFM
LDTKQAROPYIGVLDIAGFEIFDYNSMEDLCI IMFTNEKLOOFFNHTMFVLSOEFYKKE
GIIWEFIDFGMDLAACIELIEKPMGIFSILEECMFPKASDVTFKNKLFDQHLGKNRA
FEKPKPAKDKAEAHFSLVHYAGTVDYNTGWLDKNKDPLNDSVIGLYQKSSNKLLFYL
YEPVVEBVGGAKKGGKKGGSMOTVSOFTENBLGKLMTNLASTHPHFVRCLIPNESKT
PGLMENHLVIHQLRCNGVLEGIRICTKGFPSRIIYADFKQRYKVLNASVIPOGQFIDN
KKASEKLLGSIDVPHDEYKFGHTKVFFKAGLLGTLGTLEBMRDEKLALVGMIOAAGRGYV
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AKSDENARQVNDISAQRARLLTENG"
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IQLEAKYKETPERLEDEELINAELTAKKKKLEDECSELKKDIDDLELTLAKYEKEKA
ICHEAKYKETPERLEDEELINAELTAKKKKLEDECSELKKDIDDLELTLAKYEKEKA
TENKYKNLTEEMASQDESVAKLTKEKKALGESHQQTLDDLQAEEDKYNTLTKAKTKLE
QQVDDLEGSLEQEKKLAMDLEBSKRKLEGDLKLAQETYMDLENDKOQSDEKIKKKDFE
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SLEDQIIAANPLLEAYGNAKTVRNDNSSRFGKFIRIHFHANGKLSSADIETYLLEKSR
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VLYNLAERYAAWMIYTYSGLECATVNPYKWLPYYDQSCVNAYRGKKRMEAPPHIFSVS
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/protein_id="BAA33452.1"
/db_xref="GI:3668187"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /organism="Theragra chalcogramma"
/db_xref="taxon:48550"
/tissue_type="skeletal muscle"
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Borrelia
AE001138
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Fraser, C.M., Casjens, S., Huang, W.M., Sutton, G.G., Clayton, R., Lathigra, R., White, O., Ketchum, K.A., Dodson, R., Hickey, E.K., Gwinn, M., Dougherty, B., Tomb, J.F., Fleischmann, R.D., Richardson, R.D., Ri
                                                                                           burgdorferi group.
1 (bases 1 to 11199)
                                                                                                                                                                              Borrelia burgdorferi
                                                                                                                                                                                                                                                                 Borrelia burgdorferi (section AE001138 AE000783 AE001138.1 GI:2688210
                                                                                                                                              Bacteria; Spirochaetales; Spirochaetaceae;
                                                                                                                                                                                                         Lyme disease spirochete.
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Submitted (04-SEP-2000) Molecular Cardiovascular Biology,
Submitted (04-SEP-2000) Molecular Cardiovascular Biology,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2 (bases 1 to 6298)
Sanbe, A., Gulick, J. and Robbins, J.
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/protein_id="AAG40240.1"
/db_xref="GI:11761911"
/translation="MAPKRAKKRIEGGSSNVFSMFEQTQIQEFKE"
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/strain="129/J"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Peterson, J., Kerlavage, A.R., Quackenbush, J., Salzberg, S., Hanson, M., van Vugt, R., Palmer, N., Adams, M.D., Gocayne, J., Venter, J.C. et, al.

Genomic sequence of a Lyme disease spirochaete, Borrelia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (12-DEC-1997) The Institute for Genomic Research,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Nature 390 (6660), 580-586 (1997)
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                                                                                                                                                                                                                                                                                                /note="similar to PID:1000340 GB:AE000783 percent
identity: 34.62; identified by sequence similarity;
putative"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              YFVEVVLIDVGRPLFSFPKENFLFLITLGGDGTVLLAVNLLLENENIDIPIISINMGN
VGFLADIKIEDFKKVLDRFFNNSLVINKKFLLHVTVSQHGKDLISKYALNDIIIRSSV
LNKMIYVDLMVNSESFLSYKSDGIIVSTPTGSTGYSFSAGGPILEADLEGFXLTPISP
complement(1638. .2216)
                         /gene="BB0313"
                                                                                                                                                               /product="purine-binding chemotaxis protein (cheW-1)"
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                                                                                                                                                                                                                                                                                                                                                                     complement(1064. .1594)
/gene="BB0312"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           complement(235..1116)
/gene="BB0311"
complement(235..1116)
/gene="BB0311"
                                                                          DKCEFDDIPYKDQYEE"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VSFCTDTFVKRLKNKLL"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /product="conserved hypothetical protein"
/protein_id="AAC66699.1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="similar to GB:L42023 SP:P44497 PID:1003048 PID:1221979 PID:1204329 percent identity: 33.49; identified by sequence similarity; putative"
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V"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /Organism="Borrelia burgdorferi"
/db_xref="taxon:139"
complement(77. .214)
/gene="BB0310"
                                                                                                         /translation="mfrkesskdsrsqLQvagfkigkesygvsiehirelikvpsbgvyalphvpexligTvnLrg5llpLjNLNikfGvpSl5yTeeDMLLTGYLLVKikNKLLG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HSVYNRSFVFSKLSKLSISFSKEYFIAAASIFLDGINFGSFGVDVVFEFKISSQSLNF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /gene="BB0310"
                                                                                    FVDRVLKVISFDDSRVQEPPATLQTLDRKYISGVVKLDEADNLESEYLVLIDIAKIF
                                                                                                                                                                                                                                               /transl_table=11
                                                                                                                                                                                                                                                                           /codon_start=1
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/codon_start=1
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/protein_id="AAC66705.1"
/db_xref="GI:2688224"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="hypothetical protein;
putative"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           translation="MINANLTTFPIKINMKNKVLLCINTLKSGASILGNDVKVYLETK"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    transl_table=11
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                         /note="similar to GP:1934813 percent identity: 22.14;
identified by sequence similarity; putative"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3310.
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identity: putative*
                       complement(4805. .5737)
                                                     /gene="BB0317"
                                                                                                        FPISFLIVFFEYQFFRTQEYVNSYFSLSFQFYVAIIINILVSLIKRKDRS*
                                                                                                                             /translation="MFSIFEQAIVESYLALGYLYTEKIGFLNYSIEGISYLSIFLTSF
FIYLGYGIFMSTIFTLFISFLFGFFLSFVVKKNYDIFIAGIGINIFCYFFYXYLMKSN
FNFIPGFTLMLSGNFEIFVFIAVFFIFLFITVYVISYSRIRAVFEFISSGSYEDILGE
KISSRFKSFAIFVSIFTASLAGSFIAVSLNAYSYNLGLNNGWLAICILYIAFSNPLLI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /translation="mrkitimileygliinvcpytytysikkinkkankhyieklyoks
MLLKDSKKYNKAIESLYKIINMDQNQADAHLLLSELEYLNKNWKKAIIKSQDYLKIID
FKDKKNFLDISWAYFLIGEVKNSMDYIIKFFOSGKELFRENIFIAIDALFKKSIYHFT
/gene="BB0317"
                                                                                                                                                                                                                                                                                                                                      /product="conserved hypothetical integral membrane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 complement(3998. .4804)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="hypothetical protein; identified by Glimmer;
putative"
                                                                                                                                                                                                                                                        /protein_id="AAC66695.1*
/db_xref="GI:2688214"
                                                                                                                                                                                                                                                                                                                                                                             /transl_table=11
                                                                                                                                                                                                                                                                                                                                                                                                  /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="similar to GB:L43967
identity: 26.67; identified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /gene="BB0316"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /gene="BB0316"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /product="B. burgdorferi predicted coding region BB0315"
/protein_id="AAC66704.1"
/db_xref="GI:2688223"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FNQIKNTKTTKARKEIFKLTEMINSSKSIKNSTIVALKYLNEFKNELNLYPLTNRYKN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /product="octaprenyl-diphosphate synthase (ispB)"
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/protein id="AAC6696.1"
/db_xref="G1:268215"
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YIKAPAIBIVNRGASAIHLIYGIDNSINAGNLIYFLPAKLIEKSNLKENOKLLIYENFFTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /gene="BB0314"
/note="similar to SP:P19641 GB:X68873 PID:388220
PID:606125 GB:U00096 percent identity: 33.65; ide
by sequence similarity; putative"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /codon_start=1
/transl_table=11
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YSTFLKLGVYFQIIDDIKNIKNKINGKEFGDDLLEGKKSLPIIYFLQEKKFEPKIISK
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2267. .3310
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Aspgsfsqpaykklkrgilvsdlindiglryddnfybikgdipldfyvkinfekpys
LVISDVAPKTGURLVDTSNSFULSHTIDLSLEVLLkkgnllvkvfQggdemqifkk
FEXYFKFYKKIRPKAVRKNSFBIYFLGKSFGK"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="similar to 34.36; identified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /transl_table=11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /codon_start=1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /transl_table=11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           PID:1045801 SP:P47367 percent by sequence similarity;
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AUTHORS
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ORGANISM
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VERSION
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AC017994/c
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Submitted (09-DEC-1999) Celera Genomics, 45 West Gude Drive, Rockville, MD, USA

This sequence was identified as CDM:10212930 by the submitter. For more information on this record e-mail to fly@celera.com.

* NOTE: This is a 'working draft' sequence.
                                                                                                                                                  Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
1 (bases 1 to 23091)
Adams, M. and Venter, J.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     16; Conservative
                                                                                                                                          Direct Submission
                                                                                                                                                                                                                                                                                                                                     AC017994.1 GI:6553196
HTG: HTGS_PHASE2.
                                                                                                                                                                                                                                                                                                                                                                                                                                    Drosophila melanogaster,
                                                                                                                                                                                                                                                                                                                                                                                                                     pieces
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/thanslation="mydefknivkyfpdidkpildsinlkigevkiftvvgkngegkst
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_ IIIFDESAAYFSQKEAQAFIKLLVLLKKSGYASLFITHSEITDAIKESDEFIILKOK
CFRTYNKESILSKLESSSDKVFVANINCNKFEKDPIKFNLFFEDFWKYDVSFSLNKRG
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NSSILDNFLAKFMNFENKIFIRQSYINGIKDFKKKMEFYSEEKIYRILYSKSLAFSG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /product="exported protein (tpn38b)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 complement(7194. .8246)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               complement(7194. .8246)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GTLKKFALYREMYIAKSFLICFSPLSNLDHKAYNEMSVAIRNYSKEKPVLLITSNLDE
LLLLSDNILAMKMGEVLLNVSREKISKEKLKELLFL"
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IMATGIATCAKSNSLNLGNEGQIYFGAFLVYIFSSFFGLTYFNFVFLILLSSFFYGLL
GLIPFFITFFFGLNKALTGLLISYGNQRLVDGFILNMLKTGSFSNQTKRINSLFALDS
SLIYLFLLGVSVWLFYVFIHKKTIYGLQLEILSNKKKIDIFFNINEFKYKFFAVFGSA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="similar to GB:U12861 PID:551522 percent identity:
26.33; identified by sequence similarity; putative"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /gene--"BB0319"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /product="methylgalactoside ABC transporter, ATP-binding
protein (mglA)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="similar to GB:L42023 SP:P44884 PID:1005849
PID:1220920 PID:1205071 percent identity: 32.53;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               complement(5734. .7194)
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*GI:2688212"
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*** SEQUENCING IN PROGRESS ***, in ordered
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                                                                                                                                                                                         Location/Qualifiers
1. .23091
                                                                                                                                         /organism="Drosophila melanogaster"
/db_xref="taxon:7227"
4727 c 4430 g 6787 t
                                                                   66.7%; Score 16; 100.0%; Pred. No.
                                                         0;
                                                       Mismatches
                                                                      DB 65; Length 23091; 82;
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Search completed: November 15, 2001, 06:17:26 Job time: 8011 sec

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Total number of hits satisfying chosen parameters:
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/cgn2_6/ptodata/2/ina/6B_COMB.seq:*
/cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*
/cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*
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     US-08-629-939-5
US-08-759-873-5
US-09-018-584A-6
US-09-318-982-354
US-09-385-982-354
US-08-43-731-171
US-08-755-587-20
US-08-439-814-3
US-08-439-814-1
US-08-639-814-1
US-08-639-814-1
US-08-69-9-83A-23
US-08-69-9-83A-23
US-08-69-9-83A-23
US-08-69-11-417-2
US-09-211-417-2
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US-08-687-080-55
US-09-231-47
US-08-696-731-7
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Sequence 55, Appli
Sequence 2, Appli
Sequence 7, Appli
Sequence 4, Appli
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Sequence 6, Appli
Sequence 354, App
Sequence 20, Appl
Sequence 171, App
Sequence 21, Appl
Sequence 3, Appli
Sequence 2, Appli
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Sequence 23, Appl
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; HYPOTHETICAL:
US-08-629-939-5
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Patent No. 5645995
GENERAL INFORMATION:
APPLICANT: Kieback, D
TITLE OF INVENTION: M
TITLE OF INVENTION: R
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                                                                                                                                                                          CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/629
FILING DATE: 12-APRIL-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: KIT, GORDON
REGISTRATION NUMBER: 30,764
REFERENCE/DOCKET NUMBER: A-66
TELECOMMUNICATION INFORMATION:
TELEBODNE: 2020 2020 2020
                                                                                                                                 TELEFAX: (202) 293-78 INFORMATION FOR SEQ ID NO:
                                                                                                             SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                             ZIP: 20037
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
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TELEPHONE: (202)
                                                                                TYPE: nucleic acid
                                                             STRANDEDNESS: single
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STATE: D.C.
COUNTRY: U.S.A.
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2100 Pennsylvania
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Avenue, N.W., Suite 800
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US-09-018-584A-6
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                                                                                                                                                                                                                                                           Sequence 6, Application US/09018584A Patent No. 6238863
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Best Local Similarity
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                                                                                                                                                                                                                                          GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/.
FILING DATE: 12-APRIL-1996
CLASSIFICATION: 435
COMPUTER READABLE FORM:
                                                                                                                                   APPLICANT: Bacher, Jeffery W.
TITLE OF INVENTION: IDENTIFYI
TITLE OF INVENTION: REPEAT DN
TITLE OF INVENTION: REPEAT DN
UMBER OF SEQUENCES: 147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION:
NAME: KIT, Gordon
REGISTRATION NUMBER: 30,764
                                                                                                                      CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS:
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TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS:
                COUNTRY: U.S.A. ZIP: 53711-5399
                                                                                                                                                                                                                                                                                                                                                                 96 GGCGGAGCTTGCAGTGAG 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOPTWARE: Patentin Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STREET: 2100 Pennsyr. CITY: Washington, D.C.
                                                                                                     ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                   1 ggcggagcttgcagtgag 18
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                                                                                                                                                                                                                                                                                                                                                                                                                                        18;
                                                                 Madison
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                                                  Wisconsin
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                                                                                 2800 Woods Hollow Road
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3: SUGHRUE, MION, ZINN, MACPEAK & SEAS 2100 Pennsylvania Avenue, N.W., Suite 800
                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                          Schumm, James W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     100.0%;
                                                                                                                                                   MATERIALS AND METHODS FOR IDENTIFYING AND ANALYZING INTERMEDIATE TANDEM REPEAT DNA MARKERS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           METHODS FOR DIAGNOSING AN INCREASED RISK OF BREAST OR OVARIAN CANCER
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Pred. No. 0.11;
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                                                                                                                                                                                                                                                         SEQ ID NO 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
APPLICANT: ENDEGE, WILSON O., ET AL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 354, Application US/09385982
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                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION NUMBER: US/09/385,982
CURRENT FILING DATE: 1999-08-30
                                                                                                                                                                                                                                                                                                      EARLIER APPLICATION NUMBER: 60/117,393
EARLIER FILING DATE: 1999-01-27
EARLIER APPLICATION NUMBER: 60/098,639
EARLIER FILING DATE: 1998-08-31
                                                                                                                                                                                                                                                                                                                                                                             EARLIER APPLICATION NUMBER: 09/328,111 EARLIER FILING DATE: 1999-06-08
                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION: NOVEL HUMAN GENES AND GENE EXPRESSION TITLE OF INVENTION: PRODUCTS: II FILE REFERENCE: CCDNA-260XX
                                                                                                                                                                                                                                                                    SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                       NUMBER OF SEQ ID NOS: 544
                                                                                                                                                                              LENGTH: 631
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
                                                                                                                      NAME/KEY: misc_feature
LOCATION: (1)...(631)
OTHER INFORMATION: n = A,T,C or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEPHONE: (608) 257-3501
TELEFAX: (608) 257-2275
INFORMATION FOR SEQ ID NO: 6:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IMMEDIATE SOURCE:
LIBRARY: plasmid,
CLONE: C390
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATTORNEY/AGENT INFORMATION:
NAME: Grady J. Frenchick
REGISTRATION NUMBER: 29,018
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY: Ci
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       154 GGCGGAGCTTGCAGTGAG 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OPERATING SYSTEM:
SOFTWARE: Word 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US/0 FILING DATE: 04-Feb-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 ggcggagcttgcagtgag 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRANDEDNESS: Double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDIUM TYPE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  626233
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SYSTEM: Windows 95
Word 97 (DOS text format)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Circular
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           E: Diskette - 3.5 inch, 1.44 Mb
IBM compatible PC
                                   100.0%; Score 18; DB 4; Length 631; 100.0%; Pred. No. 0.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100.0%; Score 18; DB 4; Length 471; 100.0%; Pred. No. 0.1;
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                  Mismatches
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                Indels
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RESULT 6
US-08-943-731-171
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Best Local Similarity
~~+ches 18; Conserve
                                                                                                                                                                                                                       ; NAME/KEY:
; LOCATION:
US-08-755-587-20
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Sequence 171, Application US/08943731 Patent No. 6265157
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Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                    INFORMATION FOR SEQ ID NO:
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APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS:
LENGTH: 774 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE: 25-NOV-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9523959.6
FILING DATE: 23-NOV-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: GB 96 FILING DATE: 28-AUG-1996 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                   FEATURE:
                                                                                                                                                                                                                                                                                                               FEATURE:
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                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE:
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TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                              REGISTRATION NO. 54
REFERENCE/DOCKET NUMBER: 54
                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: Kenneth D Sibley REGISTRATION NUMBER: 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: GB 99 FILING DATE: 14-DEC-1995
                                                                                                                                                                                                                                                                                                NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                       STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CITY: Raleigh
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                                                                                                                                                                                                                                                                                  LOCATION:
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o. 6045997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      INFORMATION:
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310 UCB Plaza, 3605 Glenwood Avenue, PO Drawer 31107
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Wooster, Richard I
Ashworth, Alan
                                                                                                                                             Conservative
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                                                                                                                                                                                                                                                                                 CDS
168..274
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                                                                                                                                                                                                                                      166..274
                                                                                                                                                                                                                                                                                                                                           linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        UMBER: GB 9617961.9
28-AUG-1996
                                                                                                                                                                                                                                                                                                                        DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                       double
                                                                                                                                                          100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Materials and methods relating to the identification and sequencing of the BRCA2 cancer susceptibility gene and uses thereof.
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                                                                                                                                                          Score 18; DB 3;
Pred. No. 0.099;
                                                                                                                                             Mismatches
                                                                                                                                                                         DB 3; Length 774;
                                                                                                                                            Indels
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RESULT 7
US-08-755-587-21/c
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               Sequence 21, Application US/08755587 Patent No. 6045997
                                                                                                                                                                                                    Query Match
Best Local Similarity
                                                                                                                                                                                      Matches
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                               TELEFAX: 215-567-2991
TELEX: 831-494
INFORMATION FOR SEQ ID NO:
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CORRESPONDENCE ADDRESS:
ADDRESSEE: PANITCH SCHWARZE JACOBS & NADEL, P.C.
STREET: ONE COMMERCE SQUARE, 2005 MARKET STREET, 22ND
STREET: FLR.
                                                                                                               MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS:
LENGTH: 863 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                     TELECOMMUNICATION INFORMATION: TELEPHONE: 215-965-1284
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US 0: FILING DATE: 03-DEC-1991
ATTORNEY/AGENT INFORMATION:
NAME: DOYLE LEARY Ph.D.,
REGISTRATION NUMBER: 36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION DATA:
APPLICATION NUMBER: 1
FILING DATE: 14-MAR-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: ALA-KOKKO, LEENA, et al.

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DETECTING
TITLE OF INVENTION: ALTERED TYPE I OR TYPE IX COLLAGEN GENE SEQUENCES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE: 14-MAR-1994 PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                     TOPOLOGY:
                                                                                                                                                                                                                                                                                                                    TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: IBM PC
OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY: USA
ZIP: 19103-7086
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                                                                                                                                                                                  Conservative
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SPOTILA, LORETTA D.
DELTAS, CONSTANTINOS D.
SEREDA, LARISA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COLIGE, ALAIN EARLY, JAMES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PACK, MICHAEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LARSON, ANDREA W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Floppy disk
                                                                                                                                                                                                                                                                                   DNA (genomic)
                                                                                                                                                                                                  100.0%;
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                                                                                                                                                                                                Score 18; DB 4; Length 863; Pred. No. 0.098;
                                                                                                                                                                                  Mismatches
                                                                                                                                                                                Indels:
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APPLICANT: APPLICANT: APPLICANT:

Stratton, Michael R Wooster, Richard

Ashworth, Alan

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US-08-755-587-21
                                                                                                                                                                                                Sequence 3, Applic Patent No. 5968735
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REFERENCE/DOCKET NUMBER: 5
INFORMATION FOR SEQ ID NO: 21:
SEQUENCE CHARACTERISTICS:
                                                                                                             APPLICANT: STEIN, Ulrike
APPLICANT: WALTHER, Wolfgang
TITLE OF INVENTION: VECTOR FOR THE EXPRESSION OF
TITLE OF INVENTION: THERAPY-RELEVANT GENES
                                                                                      CORRESPONDENCE ADDRESS:
                                                                                                      NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                FEATURE:
NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DALE.
ATTORREY/AGENT INFORMATION:
NAME: Kenneth D Sibley
"""" TEMPARTON NUMBER: 31,665
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE: 14-DEC-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 96
FILING DATE: 28-AUG-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION NUMBER: GB 9523959.6
FILING DATE: 23-NOV-1995
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION DATA
COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS:
                                         ADDRESSEE: NIKAIDO, MARMELSTEIN, STREET: 655 Fifteenth Street, N. STREET: Street Lobby
                                                                                                                                                                                                                                                                                              29
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                                                                                                                                                                                                                                                                                                                                                        Local Similarity
nes 18; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LOCATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US/08/755,587 FILING DATE: 25-NOV-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME/KEY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE:
                                                                                                                                                               INFORMATION:
CANT: STEIN, Ulrike
                           Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  nucleic acid
                                                                                                                                                                                                            Application US/08439814
                g
 USA
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310 UCB Plaza, 3605 Glenwood Avenue, PO Drawer 31107
                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CDS
502..550
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501..550
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Pred. No. 0.
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                                                     MURRAY & ORAM W., Suite 330
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Version #1.25 (EPO)
                                                                                                                                                                                                                                                                                                                                                                DB 3;
0.096;
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US-08-439-814-2:
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                                                                                                                                                                                                                            GENERAL INFORMATION:
APPLICANT: STEIN, Ulrike
COUNTRY: USA
ZIP: 20005-5701
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                    APPLICANT: STEIN, ULLING APPLICANT: STEIN, WOLFGANG APPLICANT: WALTHER, WOLFGANG THE EXPRESSION OF TITLE OF INVENTION: THERAPY-RELEVANT GENES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE: 10-NOV-1993
INFORMATION FOR SEQ ID NO: 3
                                                                                                                                              CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY: 11
MOLECULE TYPE:
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APPLICATION NUMBER: 1
FILING DATE: 10-NOV-
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MEDIUM TYPE: Floppy disk
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: DE PCT/DE93/01086 FILING DATE: 10-NOV-1993 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: DE P 4238778.7
FILING DATE: 12-NOV-1992
PRIOR APPLICATION DATA:
                                                                       CITY:
STATE:
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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                                                                                                  STREET:
                                                                                                                 STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity
mes 18; Conserv
                                                                                                                                  ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0, Version #1.30B (EPO)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                         1 ggcggagcttgcagtgag 18
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FILING DATE: 12-NOV-1992
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TELEFAX: 202/638-4810
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REFERENCE/DOCKET NUMBER: P1614-5015
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: FILING DATE: 12-MAY
                                                                                                                                                                                                                                                                                                                                                          GGCGGAGCTTGCAGTGAG 22
                                                                  Washington
DC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               nucleic acid
DEDNESS: single
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                                                                                                                                                                                                                                                                          Application US/08439814
                                                                                                    Street Lobby
                                                                                                         E: NIKAIDO, MARMELSTEIN, MURRAY & ORAM LLP 655 Fifteenth Street, N. W., Suite 330 G
                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        linear
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Pred. No. 0.094;
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
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FILING DATE: 12-NOV-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT
FILING DATE: 10-NOV-1993
INFORMATION FOR SEQ ID NO: 2:
                                                                                                                                                                           APPLICANT: Patel, Divyen
TITLE OF INVENTION: A NITH
TITLE OF INVENTION: (NBMP)
TITLE OF INVENTION: PROTEJ
TITLE OF INVENTION: USE
                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                            APPLICANT:
APPLICANT:
                                                                                                                                                CORRESPONDENCE ADDRESS:
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MEDIUM TYPE: Floppy disk
                                                                                                                                                                NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                 375
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PRIOR APPLICATION DATA:
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ATTORNEY/AGENT INFORMATION:
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APPLICATION NUMBER:
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                                                                                                STREET: 411 H
STREET: Floor
                                                  COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: KLESNER, Sharon N.
REGISTRATION NUMBER: 36,335
REFERENCE/DOCKET NUMBER: P1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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FILING DATE: 12-NOV-1992
                                                                                                                                 ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                            GGCGGAGCTTGCAGTGAG 392
                                      07601
                                                                                    Hackensack
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1: 1688 base pairs nucleic acid
                                                                 New Jersey
                                                                                                                                                                                                                                                                                                                              Application US/09058389A
                                                                                                                411 Hackensack Ave,
                                                                                                                                                                                                                                                              Crawford, Charles R.
                                                                                                                                                                                                                                                                                 Belt,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                    USA
                                                                                                                              David A. Jackson,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              linear
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                                                                                                                                                                                                                                                                                 Judith A.
                                                                                                                                                                                           A NITROBENZYLMERCAPTOPURINERIBOSIDE (NBMPR)-INSENSITIVE, EQUILIBRATIVE, PROTEIN, NUCLEIC ACIDS ENCODING THE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 18; DB 2; Length 1688; Pred. No. 0.092;
                                                                                                           , Esq.
Continental Plaza, 4th
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                         NUCLEOSIDE TRANSPORT
SAME AND METHODS OF
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RESULT 11
US-08-439-814-1
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Best Local Similarity
Watches 18; Conserve
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; HYPOTHETICAL:
US-09-058-389A-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 1,
                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
                                                                                       FILING DATE: 12-MAY-1
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
                                                                                                                                 SOFTWARE: Patentin ker
CURRENT APPLICATION DATA:
APPLICATION NUMBER: USA
                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: STEIN, WALTHER, WOLIGANG
APPLICANT: WALTHER, WOLIGANG
TITLE OF INVENTION: VECTOR FOR THE EXPRESSION OF
THERAPY-RELEVANT GENES
FILING DATE: 10-NOV-1993
ATTORNEY/AGENT INFORMATION:
                              APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REFERENCE/DOCKET NUMBER: 13
TELECOMMUNICATION INFORMATION: 201-487-5800
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CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                 STREET:
                                                             APPLICATION NUMBER: DE P
FILING DATE: 12-NOV-1992
                                                                                                                                                                                       COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                       COMPUTER:
                                                                                                                                                                                                                                                 COUNTRY: USA
ZIP: 20005-5701
                                                                                                                                                                                                                                                                                     STATE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GGCGGAGCTTGCAGTGAG 439
                                                                                                                                                                                                                                                                                                Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         nucleic acid
                                                                                                                                                                                                                                                                                   В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Application US/08439814
                                                                                                                                                                                                                                                                                                               SE: NIKAIDO, MARMELSTEIN, MURRAY & ORAM LLP
655 Fifteenth Street, N. W., Suite 330 G
Street Lobby
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1712 base pairs
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                                                                                                                                                                     PatentIn Release #1.0, Version #1.30
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/desc = "intron 2"
                                                                                                                         12-MAY-1995
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            double
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                              DE PCT/DE93/01086
                                                                            DE P 4238778.7
                                                                                                                                      US/08/439,814
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Pred. No. 0.091;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 1712;
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NAME: KLESNER, Sharon REGISTRATION NUMBER: 3

INFORMATION:

36,335 Pa- P1

P1614-5015

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Patent No. 608408
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INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
                                                                                                                                                                          CLASSIFICATION DATA:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/609,583
FILING DATE: 01-MAR-1996
APPLICATION NUMBER: US 08/487,748
PRICTURE DATE: 07-JUN-1995
PRICTURE DATE: 07-JUN-1995
PRICTURE DATE: 07-JUN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: WO PCT/DE93/01086 FILING DATE: 10-NOV-1993 INFORMATION FOR SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                             OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ Version 2.0
CURRENT APPLICATION DATA:
                                                   TELECOMMUNICATION INFORMATION: TELEPHONE: 212-790-9090
                                                                                                                                       FILING DATE: 03-MAR-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION DATA:
APPLICATION NUMBER: DE P4238778.7
FILING DATE: 12-NOV-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES: 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                777 GGCGGAGCTTGCAGTGAG 794
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ITLE OF INVENTION:
                                      TELEFAX:
                                                                                      REFERENCE/DOCKET NUMBER:
                                                                                                        REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US/08/829,525
FILING DATE: 28-MAR-1997
                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: PatentIn Release #1.0, Version #1.30B (EPO)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 ggcggagcttgcagtgag 18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEPHONE: 202/638-5000
TELEPAX: 202/638-4810
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                                                                                                                                                                                                                                                                                                                                                                                                                                            10036/2711
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                                                                                                                       Coruzzi, Laura A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Application US/08829525
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1155 Avenue of the Americas
                                      212-869-8864
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                                                                                                                                                                                                                                                                                                                                                                                     IBM Compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pennie & Edmonds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         , Douglas A.
COMPOSITIONS AND METHODS FOR THE
TREATMENT AND DIAGNOSIS OF IMMUNE DISORDERS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
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US-08-609-583A-23/c
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
                                                                                                                                          NFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 2236 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ZIP: 10036/2711
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                               ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1472 GGCGGAGCTTGCAGTGAG 1455
                                                                                                                                                                                                                                         TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION DATA:
                                                                   EATURE:
                                                                                 OLECULE TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS:
LENGTH: 2236 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT:
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                OTHER INFORMATION:
                                                                                                                                                                                             TELEPHONE: Z12 | TELEPHONE: Z12 | 869-8864
                                                                                                                                                                                                                                                                                                                          FILING DATE: 07-JUN-1995
APPLICATION NUMBER: US 08/398,633
FILING DATE: 03-MAR-1995
                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US 08/487,748 FILING DATE: 07-JUN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: FILING DATE: 01-MA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM CON OPERATING SYSTEM:
                                                 NAME/KEY:
                                                                                                            STRANDEDNESS:
                                                                                                                             TYPE: nucleic acid
                                                                                                                                                                                                                                                                            NAME: Coruzzi, Laura
REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: FastSEQ Version 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDIUM TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME/KEY: Coding Sequence
LOCATION: 42...944
OTHER INFORMATION: Human 200 gene nucleotide
OTHER INFORMATION: sequence
                                LOCATION:
                                                                                                  TOPOLOGY:
                                                                                                                                                                                                                                                               REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STREET:
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1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Levinson, Douglas A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        USA
                                Coding Sequence
                                                                                                linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Diskette
                                                                                                             single
                                                                                                                                                                                                                                                                                                                                                                                                                        01-MAR-1996
                                                                                                                                                                                                                                                                                           Laura A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TREATMENT AND DIAGNOSIS OF IMMUNE DISORDERS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPOSITIONS AND METHODS FOR THE
sequence
           Human 200 gene nucleotide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 100.0%; Score 18; DB 3; 100.0%; Pred. No. 0.089;
                                                                                                                                                                                                                                                                                                                                                                                                                                      US/08/609,583A
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US-08-609-583A-23

Query Match Best Local

Local Similarity

100.0%;

Score 18; Pred. No.

0.089; DB 4;

Length 2236;

Indels

0,

Matches

18;

Conservative

0;

Mismatches

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1472 GGCGGAGCTTGCAGTGAG 1455

1 ggcggagcttgcagtgag 18

US-08-937-399-23/c

Sequence

tent No.

23, 62882)

Application US/08937399

ENERAL INFORMATION:

APPLICANT: Levinson,
TITLE OF INVENTION: O NUMBER OF SEQUENCES:

, Douglas A.
COMPOSITIONS AND METHODS FOR THE
TREATMENT AND DIAGNOSIS OF IMMUNE DISORDERS

CORRESPONDENCE ADDRESS:

STREET:

1155 Avenue of the Americas

Pennie & Edmonds

ADDRESSEE:

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Query Match
Best Local Similarity
Thes 18; Conserve
           Ş
1 ggcggagcttgcagtgag 18
                              Conservative
                                      100.0%; Score 18; 100.0%; Pred. No.
                             0
                             Mismatches
                                     0.089;
                                             DB 4; Length 2236;
                            Indels
                          0;
                          Gaps
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; OTHER INFORMATION: ; OTHER INFORMATION: US-08-937-399-23

Human 200 gene nucleotide sequence

FEATURE: MOLECULE TYPE:

STRANDEDNESS: TOPOLOGY: 11

linear

single

NAME/KEY:

Coding Sequence

NFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:

0

ENGTH:

nucleic acid

TELEFAX: 212 PENNIE SEO ID N

212-869-8864

TELECOMMUNICATION INFORMATION: TELEPHONE: 212-790-9090

REFERENCE/DOCKET NUMBER: REGISTRATION NUMBER:

7853-048

ATTORNEY/AGENT INFORMATION:

'AGENT INC...
COTUZZI, Laura A.
COTUZZI, Laura A.
79

FILING DATE: 07-JUN-1995
APPLICATION NUMBER: US 08/398,633
FILING DATE: 03-MAR-1995

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Search completed: November 15, 2001, 05:55:53 Job time: 6744 sec
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                                                                                                                                                                                            ; LOCATION: US-09-031-392-1
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Patent No.
                                                                                                                         Matches
                                                                                                                                     Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                    INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION:
FILING DATE: 26-FEB-100
ATTORNEY/AGENT INFORMATION:
NAME: Meiklejohn, Ph.D., Anita L.
NAME: Meiklejohn, Ph.D., Anita L.
OT334/07
                                                                 2233 GGCGGAGCTTGCAGTGAG 2250
                                                                                                                                                                                                                                                                                                                                                          REFERENCE/DOCKET NUMBER: 07
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/542-8906
TELEPAX: 617/542-8906
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OPERATING SYSTEM: Windows95
SOFTWARE: FastSEQ for Windows Version
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1472 GGCGGAGCTTGCAGTGAG 1455
                                                                                                                                                                                                                                       FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM: MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                       TELEFAX: 01.
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                                                                                 1 ggcggagcttgcagtgag 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM CONTROL OPERATING SYSTEM:
                                                                                                                                                                                                                       NAME/KEY:
                                                                                                                                                                                                                                                              TOPOLOGY:
                                                                                                                                                                                                                                                                           STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CITY: Boston
                                                                                                                                                                                                                                                                                                     LENGTH:
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                                                                                                                                                                                                                                                                                         nucleic acid
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                                                                                                                                                                                                                                                                                                     2343 base pairs
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225 Franklin Street.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   USA
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                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Tartaglia, Louis A.
                                                                                                                                                                                                        Coding Sequence 73...1761
                                                                                                                                                                                                                                                             SS: single
linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IBM Compatible
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                                                                                                                                     100.0%;
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ENCODING GLUTEX AND USES THEREOF
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                                                                                                                                  Score 18; DB 2;
Pred. No. 0.089;
                                                                                                                        Mismatches
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                                                                                                                                               Length 2343;
                                                                                                                     Indels
                                                                                                                     0;
                                                                                                                   Gaps
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SOFTWARE: FastSEQ Version 2.0 CURRENT APPLICATION DATA:

OPERATING SYSTEM:

IBM Compatible

Sod

APPLICATION NUMBER: US/08/937,399

PRIOR APPLICATION DATA:

CLASSIFICATION: FILING DATE:

APPLICATION NUMBER: 08/609,583 FILING DATE: 01-MAR-1996

APPLICATION NUMBER:

US 08/487,748

COMPUTER READABLE FORM: MEDIUM TYPE: Diskette

10036/2711

COUNTRY:

OSA

New York